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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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     seq length:
seq length:
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Match Length
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1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*
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     GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-08-963-168C-7
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US-08-963-168C-9
US-08-963-168C-8
US-08-963-168C-8
US-08-963-168C-8
US-09-963-168C-8
US-09-911-085-2
US-09-111-085-2
US-09-376-781-5
US-09-376-781-5
US-09-232-191-5
US-09-232-191-5
US-09-232-191-37
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US-09-232-200-23
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(without alignments)
22.099 Million cell updates/sec
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14, Appl
16, Appl
7, Appl
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17, Appl
18, Appl
19, Appl
11, Appl
12, Appl
13, Appl
15, Appl
16, Appl
17, Appl
18, Appl
19, Appl
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Best Loc Matches	NUMBER O CORRESPO ADDRES STREET CITY: STATE: COUNTR COMPUTER MEDIUM COMPUT: OPERAT SOFTWAN CURRENT APPLICA FILING ATTORNEY, NAME: REGIST REFERE: REGIST REFERE: REGIST REFERE: INFORMATION SEQUENCE LENGTH TELEFA TELEFA TELETA TYPE: INFORMATION SEQUENCE LENGTH TYPE: TOPOLO MOLECULE US-08-963-168	RESULT 1 US-08-963-1 Sequence Patent No GENERAL GENERAL APPLIC APPLIC APPLIC TITLE	44444498765543211098
cal Similarity 77.8%; Pred. No. 15; 7; Conservative 0; Mismatches 2; Conservative 1;	ER OF SEQUENCES: 43 ERSPONDENCE ADDRESS: SESPONDENCE ADDRESS: A Richardson P.C. REET: 225 Franklin Street Y: Boston ATE: MA DYTER EACHABLE FORM: JTER EACHABLE FORM: JUM TYPE: Diskette APUTER: IBM Compatible ERATING SYSTEM: Windows 95 ERATING SYSTEM: Windows 95 ELICATION NUMBER: US/08/963,168C LING DATE: 03-NOV-1997 RNEY/AGENT INFORMATION: BE: Fasse, Peter J. 31STRATION NUMBER: 32,983 ERRENCE/DOCKET NUMBER: 07917/059001 DOMMUNICATION INFORMATION: LEPHONE: 617/542-5070 LEFAX: 617/542-8906 LEX: 200154 ANTON FOR SEQ ID NO: 14: ENCE CHARACTERTSTICS: NGTH: 106 amino acids E: manno acid DOCGY: linear JULE TYPE: protein 168C-14 65.5%; Score 38;	68C-14 14, Applicatic 6127166 information: ANT: Bayley. ANT: Cao, Qui ANT: Cao, Qui ANT: Wang, Yu ANT: TOVENTION:	32.5 56.0 597 4 US-09-232-201-91 32.5 56.0 597 4 US-09-232-201-99 32.5 56.0 597 4 US-09-232-201-99 32.5 56.0 597 4 US-08-847-065-16 32.5 55.2 189 1 US-07-982-650D-2 32.5 55.2 189 1 US-07-982-650D-3 32.5 55.2 196 1 US-07-982-650D-3 32.5 55.2 196 1 US-07-982-650D-5 32.5 55.2 196 1 US-07-982-650D-5 32.5 55.2 196 1 US-08-331-379-1 32.5 55.2 196 1 US-08-331-379-3 32.5 55.2 196 1 US-08-331-379-3 32.5 55.2 196 1 US-08-331-379-3 32.5 55.2 196 1 US-08-331-379-4 32.5 55.2 196 1 US-08-331-379-5 32.5 55.2 226 3 US-08-331-379-5 32.5 55.2 226 3 US-09-195-286-1 32.5 55.2 299 2 US-08-923-856-1 32.5 55.2 299 3 US-08-923-856-1 32.5 55.2 347 4 US-08-847-065-19
Indels	.h 106;		Sequence
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Gaps			91, Appl 29, Appl 21, Appli 21, Appli 22, Appli 23, Appli 24, Appli 34, Appli 34, Appli 37, Appli 37, Appli 37, Appli 38, Appli 39, Appli 39, Appli 31, Appl
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US-08-963-168C-16

GENERAL INFORMATION:

tent No.

6, Application US/08963168C 6127166

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Query Match
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Thes 7; Conserv
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                                                                                                                                                                                                                                                                                 Sequence 13,
                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
        COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                          TITLE OF INVENTION: MOLLUSCAN LINGUISTAND TITLE OF INVENTION: AND GENES ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION: 617/542-5070
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FILING DATE: 03-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, Peter J.
REGISTRATION NUMBER: 32,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                  APPLICANT: Bayley, Hagan APPLICANT: Cao, Quiping
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ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bayley, Hagan APPLICANT: Cao, Quiping APPLICANT: Wang, Yunjaun
                                                                                                                                                                                                   APPLICANT: Wang, Yunjaun
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TELEFAX: ci,
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MEDIUM TYPE: Diskette
                                                                          STATE: MA
                                                                                       STREET: 225 P
CITY: Boston
 COMPUTER:
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                                                                                                                          ADDRESSEE:
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02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                          225 Franklin Street
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IBM Compatible
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                                                                                                                                                                                     MOLLUSCAN LIGAMENT POLYPEPTIDES
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08963168C Patent No. 6127166
                                                                                                                                        OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/963,168C
FILING DATE: 03-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: FASSE, Peter J.
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/059001
TELEPHONE: 61/242-5070
                                                                                             TELEX: 200154
INFORMATION FOR SEQ ID NO:
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/963,168C
FILING DATE: 03-NOV-1997
                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
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NAME: Fasse, Peter J.
REGISTRATION NUMBER: 32,983
MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: MOLLUSCAN LIGAMENT POLYPEPTIDES
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CITY: Boston
STATE: MA
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                                 TOPOLOGY:
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OPERATING SYSTEM:
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emreem: 225 Franklin Street
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                             linear
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internal
              protein
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77.8%;

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Best Local S
Matches 7
                                                   Sequence 6, Application US/08963168C Patent No. 6127166
GENERAL INFORMATION:
APPLICANT: Bayley, Hagan
APPLICANT: Cao, Quiping
APPLICANT: Wang, Yunjaun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/08963168C Patent No. 6127166
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Best Local S
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FBALSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/963,168C
FILING DATE: 03-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
         APPLICANT: Wang, Yunjaun
TITLE OF INVENTION: MOLLUSCAN LIGAMENT POLYPEPTIDES
TITLE OF INVENTION: AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Fasse, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cao, Quiping APPLICANT: Wang, Yunjaun
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CORRESPONDENCE ADDRESS:
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nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Fasse, Peter J. REGISTRATION NUMBER: 32,983
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OPERATING SYSTEM: Windows
                                                                                                                                                                                                          82 FGGMGGGKG 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15,
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TELEX: 200154
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/963,168C FILING DATE: 03-NOV-1997
ATTORNEY_AGENT INFORMATION:
NAME: Fasse, Peter J.
REGISTRATION NUMBER: 32,983
REFERENCE_DOCKET NUMBER: 07917/0590
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bayley, Hagan
APPLICANT: Cao, Quiping
APPLICANT: Wang, Yunjaun
TITLE OF INVENTION: MOLUSCAN
TITLE OF INVENTION: AND GENES
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE: OTHER INFORMATION: This translation is for SEQ ID NOS:1 &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/963,168C
FILING DATE: 03-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
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NAME: Fasse, Peter J.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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STREET: 25
STREET: 40
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                                                                                                                                                                                                                  COUNTRY: US
ZIP: 02110-2804
                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                   CITY: Boston
                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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Pred. No.
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                                                                                                                                                                                   TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acid
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TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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LENGTH: 111 amino acids
TYPE: amino acid
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TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/963,168C FILING DATE: 03-NOV-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bayley, Hagan
APPLICANT: Cao, Quiping
APPLICANT: Wang, Yunjaun
TITLE OF INVENTION: MOLLUSCAN LIGAMENT POLYPEPTIDES
TITLE OF INVENTION: AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 43
                                                                                                                               MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
 78
                                                                                                                                                                                                                                                                                       NAME: Fasse, Peter J.
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/059001
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les 7; Conser
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ZIP: 02110-2804
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                                                                                                                                                                        TYPE: amino acid
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                            3 FGGMGAKKG 11
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 FGGMAAKGG 86
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617/542-8906
                                                        Conservative
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77.8%;
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                                                                     Score 36; DB Pred. No. 38;
                                                        Mismatches
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RESULT 9

RESULT 11 US-09-376-781-5

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Best Local Similarity
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TYPE: PRT
; ORGANISM: Porcine retrovirus
US-09-111-085-2
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                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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LENGTH: 129
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Best Local
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APPLICANT: Miernyk, Jan A.

APPLICANT: Miernyk, Jan A.

APPLICANT: Luethy, Michael H.

APPLICANT: Luethy, Michael H.

APPLICANT: Mooney, Brian P.

APPLICANT: MOONEY BRANCHED CHAIN OXOACID DEHYDROGENASE COMPONENTS TO TITLE OF INVENTION: ENHANCE POLYHYDROXYALKANOATE BIOSYNTHESIS IN PLANTS FILE REFERENCE: UMO 1482

CURRENT FILING DATE: 1998-06-30

CURRENT APPLICATION NUMBER: 60/051,291

EARLIER APPLICATION NUMBER: 60/055,255

EARLIER APPLICATION NUMBER: 60/055,255

EARLIER FILING DATE: 1997-08-01

EARLIER FILING DATE: 1997-08-01
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                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Detection of retroviral subtypes based upon envelope TITLE OF INVENTION: Specific sequences FILE REFERENCE: 4238/75168
CURRENT APPLICATION NUMBER: US/09/111,085
CURRENT FILING DATE: 1998-07-07
EARLIER FILING DATE: 1997-05-16
NUMBER: GB 9710154.7
EARLIER FILING DATE: 1997-05-16
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Stoye, Jonathan P
APPLICANT: Weiss, Robin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.1
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231 YGGSGRKKG 239
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                                       3 FGGMGAKKG 11
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                                                                                Conservative
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66.7%;
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2.5e+02;
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Patent No. 6261806

TITLE OF INVENTION: Use
FILE REFERENCE: 61750-267
CURRENT APPLICATION NUMBER: US/09/376,781
CURRENT FILING DATE: 1999-08-18
EARLIER APPLICATION NUMBER: 60/097,015
EARLIER FILING DATE: 1998-08-18
NUMBER OF SEO ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
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US-08-560-005-4
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Pot, David A.
APPLICANT: Williams, Lewis T.
APPLICANT: Jefferson, Anne Bennett
APPLICANT: Majerus, Philip W.
TITLE OF INVENTION: No. 6001354el Grb2 Associating Protein and Nucleic
TITLE OF INVENTION: Acids Encoding Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Banerjee, Papia T. APPLICANT: Patience, Clive APPLICANT: Andersson, Goran K
                                                                                           APPLICATION NUMBER: US/08/
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Molecular Sequence of Swine Retrovirus and Methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence:PERV-A OTHER INFORMATION: polypeptide sequence taken from GenBank A OTHER INFORMATION: No. 6261806 Y12238 for comparison.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
TELEFAX: 415-326-2422
NFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                               CORRESSEE: Townsend and Townsend and Crew ADDRESSEE: Townsend and Townsend and Crew ADDRESSEE: Townsend and Tower, Suite 2000
                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH: 660
                                   REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231 YGGSGRKKG 239
                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                         ZIP: 94105
                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 FGGMGAKKG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity es 6; Conserv
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No. 6261806
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                                                                                                                                                                                                                                                                                                                                                                                California
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                                                                                               29,684
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Pred. No. 2.5e+02;
                                                                                2307K-0624000
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Best Local Similarity
Thes 6; Conserv
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US-09-418-540-4
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                                                                                                FEATURE:

NAME/KEY: Region

1.946
                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 946 amino acids
                                                                                                                                                                                                                                                       TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 17-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Jefferson, Anne Be
APPLICANT: Majerus, Philip W.
TITLE OF INVENTION: No. 62968
TITLE OF INVENTION: Acids Enc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                       LOCATION: 1..946
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
STATE: California
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TOPOLOGY: linear
                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/418,540 FILING DATE: 14-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                         TELEFAX: 415-326-2422
                                                                                                                                                                                                                                                    TELEPHONE:
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                                                                                                                                                                                                                                                                                                               NAME: Dow, Karen B.
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    Application

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               Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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66.7%;
                           60.3%;
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                                                                                       /note= "ysc5ptase"
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             Score 35; DB 4;
Pred. No. 3.6e+02;
1; Mismatches 2
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Pred. No. 3.
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APPLICANT: Stahl, Andreas
APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
FITLE OF INVENTION: Fatty Acid Transport Proteins
FILE REFERENCE: WHI97-21p3ME
CURRENT APPLICATION UMBER: US/09/232,191
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                                                                                                                                                                                US-09-232-191-5
                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-09-091-725-51
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                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/09232191 Patent No. 6284487 GENERAL INFORMATION:
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Patent No. 6329141
GENERAL INFORMATION:
APPLICANT:
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Best Local (
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FILING DATE: 23-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95203620.0
FILING DATE: 22-DEC-1995
APPLICATION NUMBER: EP 96200943.7
FILING DATE: 11-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: F VICTO POSSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acid
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||| ||:
126 KFGGPGAR 133
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nes 6; Conserv
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75.0%;
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Search completed: October 28, Job time: 13.1579 secs
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US-09-232-191-5
                                                                                                    Best Loc
Matches
                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5
LENGTH: 334
TYPE: PRT
                                                                                                                              Query Match
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                                                   26 AVEGGMGLRLKG 37
                                                               1 AKFGGMGAK-KG 11
| ||||| : ||
                                                                                                  Conservative
                                                                                                                56.0%;
66.7%;
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Pred. No. 3.4e+02;
1; Mismatches 2
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AKFGGMGAKKG 11
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Copyright (c) 1993 - 2002 Compugen Ltd
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S33852
G71097
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B72649
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C84556
T50190
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                                              AHT1 protein - yea asparaginase famil
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                                  probable hycD prot
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                                                                    ribosomal protein
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58.6	58.6	58.6	58.6	58.6	58.6	58.6	58.6	58.6	60.3	60.3	60.3	60.3	60.3	60.3	60.3
145	145	144	143	142	137	128	88	87	3512	1829	946	909	853	762	758
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S41193	R3YL16	HSUR2P	S67619	T52145	E83659	C53380	T43610	JC5035	T17121	T34239	S48433	S32538	AB2020	C71340	F71301
-	ribosomal protein	histone H2B.1, spe	ribosomal protein	ribosomal protein	hypothetical prote	polyribonucleotide	probable IS1617 tr	hypothetical prote	CPY protein - midg	hypothetical prote	inositol-1,4,5-tri	cGMP-gated cation	hypothetical prote	probable tpr prote	probable tpr prote

ALIGNMENTS

A;Reference number: A82950; MUID:20437337
A;Accession: A83341
A;Status: preliminary
A;Molecule tron.

C;Accession: A83541
R;Stover, C.K.; Pham, X.Q.;
adman, S.; Yuan, Y.; Brody,

Erwin, A.L.; M: L.L.; Coulter,

A.L.; Mizoguchi, S.D.; Coulter, S.N.; Folger, I

K.R.; Kas,

₽ .

Hickey, Larbig,

M.J.;

opportunistic

hypothetical protein PA0833 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

A83541

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A;Genetics:
A;Gene: At2g17770
A;Gene: At2g17770
                                                                                                                                                                                        R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shea, M.; Vanaken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 199
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487
A;Accession: C84556
                                                                                                                                                                                                                                                                                                                                    probable bZIP transcription factor [imported] - Arabidopsis thallana C;Species: Arabidopsis thallana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: C84556
                                                                                                                             A; Molecule type: DNA
A; Residues: 1-156 <S'
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A; Residues: 1-237 <STO>
A; Cross-references: GB:
                                                                                                                                                                    A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: strain PAO1
                                                                                                         A;Cross-references: GB:AE002093; NID:g6598809; PIDN:AAF18682.1; GSPDB:GN00139
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Best Local S
Matches 7
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  Query Match
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    65.5%;
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Pred. No.
  Score 38;
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Length 156;
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N;Alternate names: Profit?
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 03-May-1994
C;Accession: A61019
R;Schiechl, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein UU166 [imported] - Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_chang.
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C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
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A; Accession: T50190
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                                                                                                                                                                                                                                                                   A; Genetic code:
                                                                                                                                                                                                                                                                                                          A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                  A;Description: The complete A;Reference number: A82870 A;Accession: D82926
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                                                                                                    RESULT
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                                                                         17K basolateral plasma membrane protein Prot17
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Matches
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ssidues: 1-516 <BAR>
ross references: EMBL:AL133225; PIDN:CAB61769.1;
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sidues: 1-944 <GLA>
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nes 7; Conserv
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77.8%;
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Library, November 1999
                                                                                                                                                                                                                                                                                                                                                                                                                sequence
                                                                                                                                                                                                                                                                                                             GB:AF222894; NID:g6899118; PIDN:AAF30573.1; GSPDB:GN00:
; biovar 1
                                                                                                                                                                                                         Score 38; DB Pred. No. 98; 1; Mismatches
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2; Mi
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C;Keywords: iron; oxygen carrier
F;25,54,58,73,77,101,106/Binding
                                                         C; Superfamily:
                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-142 <GLA>
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Similarity 7; Conserv
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70.0%;
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               63.8%;
 Pred. No. 26;
2; Mismatches
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D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J. A;Title: Comparative genomics of Listeria species. A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 1
C;Accession: AC1102
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, E.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein A; Residues: 1-113 <UCH>
A; Residues: 1-113 <UCH>
A; Note: 3-Glu, 10-Asp, 60-Gly, 66-Asn, and 83-Gln were also found C; Comment: Hemerythrin is a respiratory protein found in several
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Histochemistry 93, 513-518, 1990
A; Title: N-terminal amino acid sequence,
A; Reference number: A61019; MUID: 90236771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein Seq. Data Anal. 3, 141-147, 1990
A;Title: The amino acid sequence of hemerythrin
A;Reference number: JT0556; MUID:90301732
A;Accession: JT0556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Siphonosoma cumanense
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992
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                                                                                                                                     A;Cross-references: GB:NC_003210; PIDN:CAD00745.1; A;Experimental source: strain EGD-e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polyribonucleotide nucleotidyltransferase domain present [imported] - Listeria monocy
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                                                                    polyribonucleotide nucleotidyltransferase homolog
Score 37;
Pred. No. 2
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                                                                                                                                                             PID:g16409583; GSPDB:GN00177
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Entian, K.D.; I
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heat shock
C; Species:
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S41758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acyl-CoA dehydrogenase (acd-3) [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
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E90373
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A; Residues: 1-142 <GLA>
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A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.

eference number: AB1077; MUID:21537279; PMID:11679669

cession: AC1464
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R;Glaser, P.; Erangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.;
.: Dominquez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; !
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C;Superfamily: acyl-CoA
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A;Experimental source: strain Clipl1262
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A; Residues: 1-371 <KUR>
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;Date: 27-Nov-2001 #sequence_revision
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protein dnaJ - Clostridium
Clostridium acetobutylicum
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7; Conser
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Pred. No.
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                   acetobutylicum
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Medina, N.; Peng, X.; Thi-Ngoc,
Van der Oost, J.
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goc, H.P.; Redder,
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Fsihi, H.
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RNA helicase - fruit fly (Drosophila C;Species: Drosophila melanogaster
                 S11485
RNA helicase
                                                       RESULT 12
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R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001

A; Title: Genome Sequence and Comparative Analysis of the Solve A; Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         molecular chaperones DnaJ (HSP40 family) [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001 C;Accession: C97058
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C; Accession:
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A; Residues: 1-374 < KUR>
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A; Residues: 1-72 <NAR>
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A; Residues: 1-374 <BEH>
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87.5%;
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Bahl, H.
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ATCC824
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melanogaster)

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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-575 < DOR>
A; Cross-references: EMBL: X52846; NID: g8443; PIDN: CAA3703'
C; Genetics:
A; Gene: FlyBase: Rm62
A; Cross-references: FlyBase: FBgn0003261
C; Superfamily: ATP-dependent RNA helicase DBP1
C; Superfamily: ATP-dependent RNA helicase DBP1
C; Keywords: ATP; nucleotide binding motif A (P-loop)
F; 181-188/Region: nucleotide-binding motif B
F; 287-292/Region: nucleotide-binding motif B
RESULT 14
$33852
hydrogenase
C; Species: W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N;Alternate names: pap pili
C;Species: Escherichia coli
C;Species: Bs-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Jul-1999
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Jul-1999
C;Accession: A23221; S25216; A05229; S16395
R;Baga, M.; Normark, S.; Hardy, J.; O'Hanley, P.; Lark, D.; Olsson, O.; Sch
J. Bacteriol. 157, 330-33, 1984
A;Title: Nucleotide sequence of the papA gene encoding the pap pilus subuni
A;Reference number: A91794; MUID:84087728
A;Accession: A23221
                                                                                                                                                                                                                                                                                                    C;Superfamily: F7-2 fimbrial protein
C;Keywords: fimbria
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A; Experimental source: strain
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·23-185/Product: fimbrial protein papa
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Best Local
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A.; Baga, M.;
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M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophili A;Reference number: A71000; MUID:98344137
A;Accession: G71097
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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G71097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: hydrogenase (NiFe) small chain C;Keywords: 4Fe-4S; metalloprotein; oxidoreductase C;Keywords: 4Fe-4S; metalloprotein; oxidoreductase F;85,88,185,218/Bhidning site: 4Fe-4S cluster (His, F;256,259,284,290/Binding site: 4Fe-4S cluster (His,
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C;Accession: G71097
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A; Residues: 1-387 <KAW>
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C;Species: Pyrococcus horikoshii
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A; Residues: 1-386 < DRO>
Search completed: October
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AHTI YEAST
RA55_SCHPO
CH6B_DROME
CNG4_HUMAN
YIA2_YEAST
YQ14_BACSU
RS16_CANAL
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HEMT_SIPCU
DNAJ_CLOAB
RM62_DROME
DLP4_HUMAN
PAPA_ECOLI
MBHS_WOLSU
DLP4_RAT
RS19_MYCCA
RL3_PLARO
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P22766 siphonosoma
P30725 clostridium
P19109 drosophila
O9y2h0 homo sapien
P04127 escherichia
P29589
P29789
P39789
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P04127
P31884
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fritillaria
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gossypium h
lupinus pol
arabidopsis
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mus musculu
arattus norv
secherichia
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3 planobispor
9 saccharomyc
9 schizosacch
5 drosophila
8 homo sapien
9 saccharomyc
8 bacillus su
10 bacillus su
10 candida alb
10 tortula rur
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NDARD; 19, Cre 19, Las 36, Las nse. ; Sipun	65.5 y 70.0 rvative 1	1057 107	itry in	.A. 9; PubMed=1104872 kowitz E.J., Glas equence of the mu 762(2000).	(Ure es; Urea	40, Creat 40, Last 40, Last 40, Last ein UU166	STANDARD;		428 1221 1267 1723 140 144 144 145 226 382 395
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113 AA. e update) ion update) ipunculidae; Siphonosoma	; DB 1; Length . 40; tches 2; Inde	C99B8274 CRC64	s produced thr matics and the There are no 19 as its control of Usage by see http://www.	S., Heiner C.R., Ch l pathogen Ureaplas	ticum biotype 1) ridium group; M	update) on update)	944 AA.	MENTS	
soma.	••		- sidiri	en ε.). Ollicutes				Q9kf52 P12531 Q04217 Q04217 Q9z812 Q22054 P14131 P17008 P96985 P43735 P43735 P943735
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RESULT 3
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P30725;
01-APR-1993 (Rel. 3
01-NOV-1995 (Rel. 3
16-OCT-2001 (Rel. 4
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J.
                                              SEQUENCE FROM N.A.

STRALM-ATCC 824 / DSM 792 / VKM B-1787;

MEDLINE-21359325; PubMed=11466286;

MOELLINE J., Breton G., Omelchenko M.V., Makar Gibson R., Lee H.M., Dubois J., Qlu D., Hitti Tatusov R.L., Sabathe F., Doucette-Stamm L., Sennett G.N., Koonin E.V., Smith D.R.;
                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-ATCC 4259 / DSM 1731 / NCIB
MEDLINE-94123950; PubMed-7507453;
                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Clostridium.
                                                                                                                                                                                                                                                                                                                        Chaperone protein DNAJ OR CAC1283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT
VARIANT
VARIANT
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VARIANT
                        "Genome sequence and comparative analysis bacterium Clostridium acetobutylicum.";
                                                                                                                                                          Behrens S., Narberhaus F., Bahl H.; "Cloning, nucleotide sequence and structural analysis "Clostridium acetobutylicum dnaJ gene"; EMS Microbiol. Lett. 114:53-60(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01814; Hemerythrin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE.
MEDLINE=90301732; PubMed=2362933;
Uchida T., Yano H., Satake K., Ku
                                                                                                                                                                                                                                                                   NCBI_TaxID=1488
                                                                                                                                                                                                                                                                                                          Clostridium acetobutylicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ochida T., Yano H., Satake K., Kubota I., Tsugita A.;
"The amino acid sequence of hemerythrin from Siphonosoma cumanense.";
Protein Seq. Data Anal. 3:141-147(1990).
-1- FUNCTION: HEMERYTHRIN IS A RESPIRATORY PROTEIN IN BLOOD CELLS OF
CERTAIN MARINE WORMS. THE OXYGEN-BINDING SITE IN EACH CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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             Bacteriol.
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SUBUNIT: HOMOTRIMER.
SIMILARITY: BELONGS TO THE HEMERYTHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKYGGYGAHK 74
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7; Conserv
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             183:4823-4838(2001)
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annotation
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Pred.
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Tron
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ON 1 (BY SIMILARITY).
ON 1 AND 2 (BY SIMILARITY).
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ON 2 (BY SIMILARITY).
ON 1 AND 2 (BY SIMILARITY).
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on update)
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Hitti J., Wolf Y
m L., Soucaille P
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RM62_DROME STANDARD; P19109; Q9VNK4; 01-NOV-1990 (Rel. 16, Created)

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RM62_DROME
                                                                                                              Query Match
Best Local
                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00636; DNAJ_1; 1.
PROSITE; PS50076; DNAJ_2; 1.
PROSITE; PS00637; DNAJ_CXXCXGXG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X69050; CAA48792.1; -. EMBL; AE007640; AAK79254.1; -. EMBL; M74569; AAA23247.1; -.
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- FUNCTION: ACTS AS A CO-CHAPERONE. STIMULATES, JOINTLY WITH THE ATPASE ACTIVITY OF DNAK (BY SIMILARITY).

- COPACTOR: BINDS TWO ZINC IONS PER MONOMER (BY SIMILARITY).
                                                                                                                                                                METAL
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REPEAT
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Pfam; PF01556; DnaJ_C; 1.
Pfam; PF00684; DnaJ_CXXCXGXG;
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HSSP; P25685; 1HDJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acetobutylicum, including grpE, dnaJ, and J. Bacteriol. 174:3290-3299(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Narberhaus F., Giebeler K., Bahl H.; ^{\prime\prime} Molecular characterization of the dnaK gene region of Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-72
STRAIN-ATCC 4259
                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00271; DnaJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002939;
InterPro; IPR001305;
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                                                 154
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                                                                   4 GGMGAKKG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
INDUCTION: BY HEAT SHOCK.
SIMILARITY: BELONGS TO THE DNAJ FAMILY.
SIMILARITY: CONTAINS 1 J DOMAIN.
SIMILARITY: CONTAINS 1 CR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                 GGTGAKKG 161
                                                                                                              Similarity
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150
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                                                                                                                                                                                                                                                                                                                                                    replication;
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/ DSM 1731 /
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87.5%;
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DnaJ_CXXCXGXG.
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EMBL; AE003601; AAG22212.1; ALT_INIT. PIR; S11485; S11485.

DEAD_ATP_helicase. Helicase_C

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RA Fosler C., Gabrielian A.E., Garge N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Hewland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Hostin S.M., Moy M., Murphy B., Murphy L., Muzpy D.M., Nelson D.L.,
RA Meint S.M., Moy M., Murphy B., Murphy L., Muzpy D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhoo Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Rubin G.M., Venter E.,
Subcellular Locarion. Nuclear (Potential).

CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.
Durbin K.J., Evangelista C.C., Ferrac C., Ferriera S., Fleischmann W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballow B.D., Bayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballow B.D., Bayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; A
Pterygota; Neoptera;
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Drosophilidae; Dro
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use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its or send an email to license@isb-sib.ch). as its content http://www.isb-sib.ch/announce/ Usage γď and for commercia no

SUBFAMILY.

EMBL; X52846; CAA37037.1; AE003601; AAF51926. AAF51926.1; AAG22213.1;

SIMILARITY: BELONGS TO THE DEAD ALT_INIT BOX HELICASE FAMILY. DDX5/DDX17 H.O., ₹... DLP4_HUMAN
ID DLP4_H
AC Q99Y2HO
DT 16-OCT
DT 16-OCT
DT 01-MAR
DE DISKS
DE PYOCLEI
GN DLGAP4
OS HOMOO SE
CO EUKARY
OC MAMMAI
OX NCB1_T
RN GISUEN
RX MEDLIN
RX DAILey
RX DAILey
RX Basle
RX Clagg
RX Clagx
RX HAMMON
RX LENVAS
RX MINSh
RX 밁 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RP Deloukas P., Matthews L.H., Ashrust J., Burton J., Gilbert J.G.R.,

A Dones M., Stavrides G., Almelda J.P., Babbage A.K., Bagguley C.L.,

RA Jones M., Stavrides G., Almelda J.P., Babbage A.K., Bagguley C.L.,

RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,

RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,

RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,

RA Chapman J.C., Collier R.E., Connor R., Corby N.R.,

RA Cliegy S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,

RA Coulson A., Coville G.J., Deadman R., Dhami P., Dunn M.,

RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,

RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,

RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,

RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

RA Marsh V.L., Martin S.L., McConnachle L.J., McLay K., McMurray A.A.,

RA Marsh V.L., Martin S.L., McConnachle L.J., McLay K., McMurray A.A.,

Detail B. Detail B. D., McConnachle L.J., Nickerson T.,

Detail B. D., Detail B. D., Detail B. D., Detail B. D.,

RA Cliver B. D., Detail B. D., Detail B. D., Detail B. D.,

RA Cliver B. D., Detail B. D., Detail B. D., Detail B. D.,

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RA C., D., D., D., D., D., D., D.,

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RA C., D., D., D., D., D. RESULT Matches Query Match Best Local : InterPro; IPR001410; DEAD.
InterPro; IPR000529; DEAD_ATP_}
InterPro; IPR001550; Helicase_C
Pfam; PF00270; DEAD; 1.
Pfam; PF00271; helicase_C; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1. Q9YZH0; Q9HIL7; Q9HI37; Q9HI30;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update) DOMAIN CONFLICT CONFLICT SEQUENCE NP_BIND Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "prediction of the coding sequences of unidentified human The complete sequences of 100 new cDNA clones from brain w for large proteins in vitro."; DNA Res. 6:63-70(1999). Disks large-associated protein 4 (DAP-4) (SAP90/PSD-9 protein 4) (SAPAP4) (PSD-95/SAP90 binding protein 4). DLGAP4 OR DAP4 OR KIAA0964. MEDLINE=99246063; PubMed=10231032; SEQUENCE FROM N.A. (ISOFORM 1). Mammalia; Eutheria; Primates; Eukaryota; DLP4_HUMAN ATP-binding; RNA-binding; Helicase; DOMAIN 9 81 GLY-RI PROSITE; FlyBase; FBgn0003261; NCBI_TaxID=9606; Homo sapiens (Human) 542 RFGGGGFKKG 2 KFGGMGAKKG Q58083; T., Ishikawa K.-I., 7; Conserv PS00039; Metazoa; 181 291 527 51 531 575 Conservative Ä

STANDARD;

989

Chordata;

Catarrhini;

Craniata; Vertebrata; Euteleostomi;

Suyama M., Kikuno R., Hirosawa

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code

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63.8%; 70.0%;

Score 37; DB Pred. No. 38; 1; Mismatches

дв 38; <u>سر</u>

> Length 575 CRC64;

2

Indels

0

Gaps

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WW;

GLY-RICH.

R -> A (IN REF. 1).

R -> P (IN REF. 1).

R -> P (50 REF. 1).

188 294 569 51 531 52474 .

DEAD

BOX

ATP (BY SIMILARITY)

DEAD_ATP_

HELICASE; 1

Nuclear protein

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01-NOV-1986
15-DEC-1998
                                                                  Baga M., Normark S., Hardy J., O'Hanley P., Lar
Schoolnik G., Falkow S.;
"Nucleotide sequence of the papA gene encoding
of human uropathogenic Escherichia coli.";
J. Bacteriol. 157:330-333(1984).
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SEQUENCE
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                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                               Bacteria;
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EMBL; AL390374; CAC18627.1; -.
EMBL; AL050318; CAC16960.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                 NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                          Escherichia
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Nature 414:865-871(2001).
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                         EQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synapses and neuronal cell signaling. Could be an adapter protein linking ion channel to the subsynaptic cytoskeleton. May induce enrichment of PSD-95/SAP90 at the plasma membrane.

SUBUNIT: Interacts with DLG1 and DLG4/PSD-95 (By similarity).

SUBCELLULAR LOCATION: Membrane-associated (By similarity).

ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be produced by alternative splicing.

SIMILARITY: BELONGS TO THE SAPAP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                      fimbrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: May play a role in the molecular organization
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S., Hardy J., O'Hanley
                                                                                                                                                                                                                                                                                                                                                                                                                 03, Created)
03, Last sequence update)
37, Last annotation update)
r pilin protein precursor (P
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70.0%;
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                                                                                                                                                                                                                                                                                                                                            gamma subdivision; Enterobacteriaceae;
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Pred. No.
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There are no restrictions on ong as its content is in no
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                                                                                                                                                                   Lark D.,
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                                                                                                                                                                   Olsson O.,
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          The quinone-reactive Ni/Fe-hydrogenase Eur. J. Biochem. 206:93-102/1007
                                                                                                                                                   Wolinella
Bacteria;
                                                                                                                                                                                                  01-JUL-1993 (Rel. 26, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Quinone-reactive Ni/Fe-hydrogenase small chain pr
(EC 1.12.99.3) (Membrane-bound hydrogenase small
                                                                                                                                                                                                                                                                                                 WOLSU
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
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                                                        MEDLINE-92267032; PubMed=1587288;
Dross F., Geisler V., Lenger R.,
Fahrenholz F., Kojro E., Duchene
                                                                                                                                                                                                                                                          P31884;
01-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     operons as a mechanism for the adhesive properties.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marklund B.-I., Tennent J.M., Garcia E., Hamers A., Baga M., Lindberg F., Gaastra W., Normark S.; Thorizontal gene transfer of the Escherichia coli pap and prs operons as a mechanism for the development of tissue-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                               SEQUENCE FROM N.A.,
                                                                                                                          NCBI_TaxID=844;
                                                                                                                                         Wolinella
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                                                                                                                                                                                          Hydrogen:quinone oxidoreductase).
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DISEASE: STRAINS OF E.COLI THAT CAUSE INFECTION OF THE HUM.

DISEASE: STRAINS OF E.COLI THAT CHICA ARE HAIR-LIKE APPENDAY.

URINARY TRACT PRODUCE PAP-PILI WHICH ARE HAIR-LIKE APPENDAY.

CONSISTING OF ABOUT 1000 HELICALLY ARRANGED SUBUNITS OF TH

PROTEIN PAPA. THESE PILI MEDIATE BINDING TO DIGALACTOSIDE-
CONTAINING GLYCOLIPIDS PRESENT ON THE EPITHELIAL CELLS WHIT

LINE THE URINARY TRACT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . Microbiol. 6:2225-2242(1992). FUNCTION: FIMBRIAE (ALSO CALLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE FIMA/PAPA FAMILY OF FIMBRIA PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A23221; YQECPP.
rPro; IPR000259; Fimbrial.
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                                                                                                                                                  succinogenes.
Proteobacteria;
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185
83
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87.5%;
                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAP FIMBRIAL MAJOR PILIN PROTEIN.
                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                        Theis F., KI
A., Tripier
                                                                                                  QF
                                                                                                                                                     subdivision;
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                                  Wolinella succinogenes.";
                                                                        Krafft
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                                                         D., Juvenal
                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 185;
                                                                                                                                                     Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                                                                      subunit)
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Best Local S
Matches 7
                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
D1sks large-associated protein 4 (DAP-4) (SAP90/PSD-95-associated protein 4) (SAPAP4) (PSD-95/SAP90 binding protein 4).
DLGAP4 OR DAP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
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InterPro; IPR001821; N1Fehydrog_small.
Pfam; PF01058; oxidored_q6; 1.
PRINTS; PR00614; NIHGNASESMLL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- CATALYTIC ACTIVITY: H(2) + menaquinone = reduced menaquinone
-1- COFACTOR: CONTAINS NICKEL AND IRON-SULFUR.
-1- SUBUNIT: HETERODIMER OF A LARGE AND A SMALL SUBUNIT.
                                                                                                                                                                                       TISSUE-Brain;
                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                            DLP4_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oxidoreductase; Signal; Membrane; Iron-sulfur; Nickel SIGNAL 1 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X65189; CAA46302.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SUBCELLULAR LOCATION: Membrane-bound.
-1- SIMILARITY: TO OTHER UPTAKE HYDROGENASES SMALL SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kroeger A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dross F., Geisler V., Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93307313; PubMed=8319698;
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
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SWISS-PROT entry is copyright.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354 AA;
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                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                    Chordata;
Rodentia;
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70.0%;
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Pred. No.
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                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C39CC21D2F5AB7D0 CRC64;
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produced through a collaboration
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Pfam; PF00203; Ribosomal_S19; 1.
PRINTS; PR00975; RIBOSOMALS19;
ProDom; PD001012; Ribosomal_S19; 1.
PROSITE; PS00323; RIBOSOMAL_S19; 1.
Ribosomal protein; rRNA-binding.
SEQUENCE 88 AA; 9903 MW; 1BF2AC24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-1989
01-MAR-1989
01-OCT-1994
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the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                         EMBL; X06414; CAA29708.1; -. PIR; S02835; R3YM19. HSSP; P80381; 1QKF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohkubo S., Muto A., Kawauchi Y., Yamao F., Osawa S.;
"The ribosomal protein gene cluster of Mycoplasma capricolum.";
Mol. Gen. Genet. 210:314-322(1987).
-i- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STI
TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-ATCC 27343 / KID;
MEDLINE-88142549; PubMed-3481422;
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76
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mal protein S19.
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01-NOV-1997
30-MAY-2000
                                                                                                                                                                                                                                 YEAST
                                                                                                                                  AHT1_YEAST STANDARD; PRT; 182 AA P29589; P38807; Created) 01-APR-1993 (Rel. 25, Created) 01-FEB-1995 (Rel. 31, Last sequence update) 01-FEB-1995 (Rel. 31, Last annotation update) Hexose transport activator protein. AHT1 OR YHRO93W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
Submitted (MAY-1991)
[2]
                        SEQUENCE FROM N.A.
STRAIN-MC 971 B;
Oezcan S., Ciriacy M.;
                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00297; Ribosomal L3; 1.
ProDom; PD001374; Ribosomal L3; 1.
PROSITE; PS00474; RIBOSOMAL L3; 1.
Ribosomal protein; rRNA-binding.
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modified and this statement is not removed.
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or send an email to license@isb-sib.ch).
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P72233;
                                                                                            Eukaryota; Fungi; 
Saccharomycetales;
                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
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"An elongat
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                                                                              NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           elongation factor Tu (EF-Tu) resistant to the EF-Tu inhibitor 270 in the producing organism Planobispora rosea.";
. Microbiol. 22:43-51(1996).
FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND PARTICIPATE IN THE FORMATION OF THE PEPTIDYLTRANSFERASE CENTER THE RIBOSOME (BY SIMILARITY).
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6; Conserv
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                                                                                          Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetaceae; Saccharomyces.
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n L3 (Fragment).
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            EMBL/GenBank/DDBJ databases
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Streptosporangiaceae;
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EMBL; U00060; AAB68925.1; -
PIR; S17005; S17005.
PIR; S46717; S46717.
SGD; S0001135; AHT1.
SEQUENCE 182 AA; 19776 M
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or send a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dov Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten Kucaba T., Hillier L., Jier M., Johnston L., Langston Y., Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mo Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaug Vignat D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=S288C / AB972; MEDLINE=94378003; PubMed=8091229;
                                                                                                                                                Brown D., Churcher C.M., Wood V., Barrell B.G., Submitted (SEP-1997) to the EMBL/GenBank/DDBJ dc.i- SUBCELLULAR LOCATION: Nuclear (Potential).
-i- SIMILARITY: STRONG TO OTHER EUKARYOTIC RECA-
                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycete
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                            STRAIN-972;
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Bashkirov V.I., Khasanov
Submitted (MAR-1998) to t
                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces.
NCBI_TaxID=4896;
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RHP55 OR SPAC3C7.03C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 265:2077-2082(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
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                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
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R.,
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RA Ballaw R.M., Basu A., All H.J., Allers FlainkOch C., Bealey E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
Burtis K.C., Busam D.A., Butler H., Caddeu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Millahan N.V., Mobarry C., Morris J., Moshrefi A.,
RA Rainert K., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Syradling A.C., Stapleton M., Strong R., Sun E.,
RA Williams S.M., Woodage T., Worles O., Weitsen S.M., Wang X.,
RA Williams S.M., Woodage T., Worler E., Wang A.H., Wang X.,
RA Yel R., F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,
RA Clobs R.A., Myers E.W., Rubin G.M., Venter J.C.;
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Matches (
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EMBL; Z99568; CAB16734.1; -.
InterPro; IPR001553; RecA.
PRINTS; PR00142; RECA.
PROSITE; PS50162; RECA.2; 1
DNA damage; DNA repair; ATP-binding; Nuclear protein.
DNA damage; DNA repair; ATP-binding; Nuclear protein.
DNA damage; DNA repair; ATP-binding; Nuclear protein.
TATP (POTENTIAL).
TATP 18996 MW; 53DC65C0EC3836E1 CRC64;
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16-OCT-2001 (Rel.
Probable 60 kDa he
(Hsp60) (60 kDa cl
HSP60B OR CG2830.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20196006; PubMed=10731132
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CNG4_HUMAN
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HSSP; P06139; IGRL.
FlyBase; EBgn0011244; Hsp60B.
InterPro; IPR001844; Chaperonins_cpn60.
InterPro; IPR002423; TCP1_cpn60.
Pfam; PF00118; cpn60_TCP1; 1.
PRINTS; PR00298; CHAPERONIN60.
PRINTS; PR00304; TCOMPLEXTCP1.
                                                                                                                                                                                                                                                          Chen T.Y., Peng Y.-W., Dhallan R.S., "A new subunit of the cyclic nucleot retinal rods.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CNG4) (Cyclic nucleotide-gated cation channel modulatory subunit). CNGB1 OR CNCG4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cyclic-nucleotide-gated cation channel 4 (CNG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        014028; Q14029;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified
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                                                This SWISS-PROT
                                                                                                                                                                                                                                    Nature 362:764-767(1993).
                                                                                                                                                                                                                                                                                                                              MEDLINE=93226050; PubMed=7682292;
                                                                                                                                                                                                                                                                                                                                                           TISSUE=Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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TRANSIT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
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                                                                                                               SUBUNIT: HETEROOLIGOMERIC COMPLEX WITH CNG1.
SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; RCNC2A AND RCN
HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EW European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: PRRVENTS MISFOLDING AND PROMOTES THE REFOLDING PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER CONDITIONS (BY SIMILARITY).

SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               648 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
  ROT entry is copyright.
Swiss Institute of Bioi
Bioinformatics Institut
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Primates; Catarrhini;
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PROBABLE 60 KDA HEAT SHOCK PRO
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ATP-binding; Mitochondrion;
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Best Local :
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01-FEB-1995
01-FEB-1995
01-MAR-2002
                               SEQUENCE FROM N.A.

STRAIN-S288C / AB972;

Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,

Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,

Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,

Walsh S.V., Whitehead S.;

Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Hypothetical 108.4 kDa protein in BET1-PAN1 intergenic region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00520; ion_trans; 1.

SMART; SM00100; CNMP; 1.

PROSITE; PS00889; CNMP_BINDING_1; 1.

PROSITE; PS00889; CNMP_BINDING_2; 1.

PROSITE; PS50042; CNMP_BINDING_3; 1.
                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomyc
Saccharomycetales; Saccharomycetaceae; Sa
                                                                                                                                                                                                                                                                           YIA2_YEAST
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InterPro; IPR000595; cNMP_binding.
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CYTOPLASMIC (POTENTIAL).

H5 (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
H6 (POTENTIAL).
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H1 (POTENTIAL).
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$GD; $0001264; YIL002C.
InterPro; IPR000300; IPPC.
InterPro; IPR002013; $yja_N.
Pfam; PF00783; IPPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                               PROSITE; PS50275; SAC; 1.
Hypothetical protein; Hydrolase
DOMAIN 151 480 SAC
                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Voss H., Tamames J., Teodoru C., Valencia A., Sensen Schwager C., Zimmermann J., Sander C., Ansorge W.; "Nucleotide sequence and analysis of the centromeric
                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                      Pfam; PF02383; Syja_N; 1. SMART; SM00128; IPPC; 1.
                                                                                                                                                                                                                                                                                                                       EMBL; 238062; CAA86201.1; EMBL; X79743; -; NOT_ANNO
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              28,
              2002,
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Pred. No. 1.3e+02;
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re greater than or equal to the score of the result being printed,
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095x7 caenorhabdi
044355 aequipecten
044357 aequipecten
044354 aequipecten
044354 aequipecten
098ex7 arabidopsis
09utb5 schizosacch
                      Q917p5 drosophila
Q90wr5 lampetra fl
O44356 aequipecten
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Q97wq8 sulfolobus
Q917p5 drosophila
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007894	Q9KHF0	Q9KHF1	Q9KHF2	083337	087472	Q9UT74	Q9IUF6	041172	Q90RL8	Q961V0	093700	Q9US10	Q9нL40	Q9V2U2	Q10881	Q97VA3	Q9ABX3	Q90DY4	Q9FF85	Q9V5U5	Q04010	Q04009	6WT860	Q96WL0	Q9VGC3	Q9AJC4	Q98MA1	Q9L656
007894 treponema p	Q9khf0 treponema p		$\boldsymbol{\tau}$	533	087472 treponema p	w	o	041172 porcine end	Q90rl8 porcine end	Q961v0 drosophila	093700 sulfolobus	Q9us10 schizosacch	Q9h140 thermoplasm	Q9v2u2 methanococc	Q10881 mycobacteri	Q97va3 sulfolobus	Q9abx3 caulobacter		Q9ff85 arabidopsis	Q9v5u5 drosophila	_	Q04009 brugia mala	Q9blm9 toxocara ca	_	Q9vgc3 drosophila	Q9ajc4 chlorobium	Q98mal rhizobium l	Q91656 streptomyce

ALIGNMENTS

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RESULT 1
Q915A7
ID Q915
AC Q915
AC Q915
AC Q915
DF 01-W
DF 01-W
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DE HYPC
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RN [1]
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RM MEDLINE=20437337; pubMed=10984043;

RA HICKEY C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

RA HICKEY M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA HICKEY M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA Brody L.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

opportunistic pathogen.";

RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

opportunistic pathogen.";

RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

opportunistic pathogen.";

REMBL; ABG04518; AAG04222.1; -.

REMBL; ABG04518; AAG04222.1; -.

REMBL; ABG04518; AAG04222.1; -.

REMBL; ABG04518; AAG04222.1; -.

REMBL; ABG04518; AAG04223.1; -.

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Matches 7; Conserv
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0915A7;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
HYPOTHETICAL PROTEIN PA0833.
PA0833.
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   1 AKFGGMGAKKG 11
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                                                                     Score 39; DB Pred. No. 28; 2; Mismatches
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RESULT
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SEQUENCE FROM N.A.

MEDLINE=98044338; PubMed=9382816;
Cao Q.-P., Wang Y.-J., Bayley H.;
"Sequence of abductin, the molluscan '1
Curr. Biol. 7:0-0(1997).

EMBL; AF026846; AAB94678.1; -.

SEQUENCE 126 AA; 10593 MW; CFEED65
                                                                                                                                                                                                                                                                                                                                                044355;
01-JUN-1998
01-JUN-1998
01-NOV-1998
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Bradshaw-Cordum H.,
"The sequence of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
HYPOTHETICAL 133.3 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                          044355
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Submitted (SEP-2001) to the
EMBL; AC026301; AAK68893.1;
                                                                                                                                                                                                                                         Pectinoidea; Pectinidae; NCBI_TaxID=31199;
                                                                                                                                                                                                                                                                                 Aequipecten irradians (Bay scallop).
Bukaryota; Metazoa; Mollusca; Bivalvia;
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STRAIN-BRISTOL N2;
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cosmid Y54F10BM.";
EMBL/GenBank/DDBJ databa
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MEDLINE=98044338; PubMed=9382816;
Cao Q.-P., Wang Y.-J., Bayley H.;
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Eukaryota; Metazoa; Mollusca; Bivalvia;
Pectinoidea; Pectinidae; Argopecten.
NCBI_TaxID=31199;
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EMBL; AF026848; AAB94680.1; -. SEQUENCE 132 AA; 11103 MW; 992561
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Eukaryota; Metazoa; Mollusca; Bivalvia;
Pectinoidea; Pectinidae; Argopecten.
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EMBL; AF026845; AAB94677.1; -.
SEQUENCE 136 AA; 11365 MW; 11634DF07F935E
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Q9UTB5;
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01-MAY-2000 (TTEMBLTel. 13,
01-DEC-2001 (TTEMBLTel. 19,
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-- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-- SIMILARITY: BELONGS TO THE BZIP FAMILY.
EMBL; AF024504; AAF18682.1; --
EMBL; AF024504; AAF18682.1; --
Enterpro; IPR001871; bZIP.
Pfam; PF00170; bZIP; bZIP.
PROSTTE; PF00170; bZIP; BASIC; 1.
DNA-binding; Nuclear protein.
SEQUENCE 156 AA; 17476 MW; E4A2F76C2F068922 CRC64;
                                                                                                                                                          Barrell B.G., Rajandream M.A., McDousubmitted (NOV-1999) to the EMBL/Gen
EMBL; AL133225; CAB61769.1; -
InterPro; IPR003817; PS_Dcarbxylase.
Pfam; PF02666; PS_Dcarbxylase; 1.
SEQUENCE 516 AA; 58464 MW; FFE45
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MEDLINE-20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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        ۲.
                                                                               Length 516;
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                                                                      Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Chatrabit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Maddueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pisabarro A.G.; "Isolation and characterization of a gene of the edible basidiomycete "Isolation and characterization of a gene of the edible basidiomycete plentotus ostreatus that is homologous to CAP64 from Cryptococcus
 Transferase; Complete proteome SEQUENCE 142 AA; 15647 MW;
                       "Comparative genomics of Listeria Science 294:849-552(2001).
EMBL; AL596164; CAC95483.1; --
ListiList; LIN00250;
                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                               Listeria innocua
                                                                                                                                                                                                                                                                                                                                         POLYRIBONUCLEOTIDE
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EMBL; AJ318523; CAC5(
SEQUENCE 558 AA; 5
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Eukaryota; Fungi; Basidiomycota; Hymer
Agaricales; Pleurotaceae; Pleurotus.
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                                                                                                                                                                                                                       PubMed=11679669;
                                                                                                                                                                                                                                                                        NCBI_TaxID=1642;
                                                                                                                                                                                                                                                                                    Bacillus/Staphylococcus
                                                                                                                                                                                                                                                                                                   Bacteria;
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11262
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(TrEMBLrel. 19, Last anoctation update)
(TrEMBLRel. 19, Last anoctation update)
LEOTIDE NUCLEOTIDYLTRANSFERASE DOMAIN PRESENT.
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                                                                                                                                                                                                                                                                                    group;
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Last annotation updat
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7E4F086350AC3C49 CRC64;
                                                                                                                                                                                                                                                                                     Listeria
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                                                              species.";
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Best Local
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Sulfolobus solfataricus
Archaea; Crenarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A., De Moors A., Erauso G., Fletcher C., Gordon P.M.K., Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N., Theriault C., Tolstrup N., Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T., Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
"The complete genome of the crenarchaeon Sulfolobus solfataricus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-CCT-2001 (TrEMBLrel. 18, Created)
01-CCT-2001 (TrEMBLrel. 18, Last sequence update)
01-CCT-2001 (TrEMBLrel. 18, Last annotation update)
ACYL-COA DEHYDROGENASE (ACD-3) (EC 1.3.99.).
                                                                                             Eukaryota; Metazoa; Arthropoda; Pterygota; Neoptera; Endopterygo Ephydroidea; Drosophilidae; Dros
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-ATCC 35092 / DSM 1617 / P2;
MEDLINE-21332296; PubMed-11427726;
She Q., Singh R.K., Confalonieri F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q97WQ8
                                    STRAIN=BERKELEY;
MEDLINE=20196006; PubMed=10731132;
                                                                                 Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                    01-MAR-2001
01-DEC-2001
                                                                                                                                                                                                                   Q917P5
  George
             Adams M.D., Celn
Amanatides P.G.,
                                                             SEQUENCE FROM N.A.
                                                                                                                                 Drosophila melanogaster
                                                                                                                                              RM62 OR CG10279.
                                                                                                                                                          RM62 PROTEIN
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                                                                                                                                                                                                        Q917P5;
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PF02770;
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AE006813; AAK42244.1; -.
Pro; IPR001552; Acyl-CoA_dh.
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  R.A.,
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 Celniker S.E., Holt R.A., E
P.G., Scherer S.E., Li P.W.,
Lewis S.E., Richards S., A
                                                                                                                                                                                                                                                                                                                          Conservative
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Acyl-CoA_dh_M; 1.
Acyl-CoA_dh_N; 1.
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AA; 41394 MW; Alf
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77.8%;
                                                                                              Endopterygota; Diptera; ilidae; Drosophila.
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19,
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                                                                                                                                 (Fruit
                                                                                                                                                                    Created)
Last sequence up
Last annotation
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Pred. No. 1e+0
0; Mismatches
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                                                                                                         fly).
; Tracheata; Hexapoda; Insecta;
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             Evans C.A.,
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  Ashburner
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 R.A.,
M., H
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Gocayne J.D.,
A., Galle R.F.,
Henderson S.N.,
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RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzzny D.M., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Syler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Syler E., Spradling A.C., Stapleton M., Strong R., Yang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhi S., Zhu X., Smith H.O.
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.
RA Zheng X.H., Wars E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
R. Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local :
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Q90WR5;
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01-DEC-2001
01-DEC-2001
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                                                  KERATIN ALPHA.
Lampetra fluviatilis (River lamprey)
                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
ATP_binding; Helicase; RNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pfam; PF00270; DEAD; 1.
pfam; PF00271; helicase_C; 1.
smarT; sm00487; DEXDC; 1.
smarT; Sm00490; HELICC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- SIMILARITY: BELONGS TO THE "DEAD" BOX FAMILY HELICASE EMBL; AE003601; AAF51927.2; -. HSSP; Q58083; 1HV8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hostin D.,
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Abril J.F., Agba
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               Petromyzontiformes;
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7; Conserv
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R.C., Rogers Y.-H.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPRO01410; DEAD.
IPRO06629; DEAD_ATP_helicase.
IPRO01650; Helicase_C.
IPRO00504; RRM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ., Harvey D., Heiman T.J., Hernandez J.R., Houck J. Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
                                                                                       (TrEMBLrel. 19, (TrEMBLrel. 19, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                         578 AA;
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                 Petromyzontidae;
                                  Chordata; Craniata; Vertebrata; Hyperoartia;
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Pred. No.
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                 Lampetra
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                                                                                         update)
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SEQUENCE FROM N.A.
SEDULENCE FROM N.A.
SCHAIffeld M., Markl J.;
Schultess J., Schaffeld M., Markl J.;
Schultess J., Schaffeld M., Markl J.;
Schultess J., Schaffeld M., Markl J.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
SEMBL; ANZE89859; CAC42512.2; -
SEOUENCE 629 AA; 63326 MW; A64975CC3566F9CB CRC64;
SEOUENCE 629 AA; 63326 MW; DB 13; Length 629;
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DD1 .
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Q94DD1;
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044356;
                                                                                                                                       Oryza sativa (Rice).

Gukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

NCBI_TaxID-4530;
                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, P0683F02.21 PROTEIN. P0683F02.21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98044338; PubMed=938 Cao Q.-P., Wang Y.-J., Bayld Cao Q.-P., Wang Y.-J., the number of abductin, the number of abductin, the number of the curr Biol. 7:0-0(1997).

EMBL; AF026847; AAB94679.1;
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Eukaryota; Metazoa; Mollusca; Bivalvia;
Pectinoidea; Pectinidae; Argopecten.
NCBI_TaxID=31199;
                                                             STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic
clone:P0683F02.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998 (TREMBLRel. 06, 01-JUN-1998 (TREMBLRel. 06, 01-NOV-1998 (TREMBLRel. 08,
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EMBL; APOC
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                  tted (FEB-2001) to the EMBL/GenBank/DDBJ AP003289; BAB63718.1; -. VCE 366 AA; 40220 '''
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.-J., Bayley H.;
ctin, the molluscan 'rubber'
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11034 MW;
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77.8%;
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Pred. No. 1.8e+02;
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                          4EBFADFFA20D9DB8
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Length 366;
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Search completed: October 28, Job time: 28.4737 secs

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                                                                           pfam; PF01546; Peptidase_M20.
Hydrolase; Complete protections
                                                                                                                                                 Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H.;

"Complete sequence and gene organization of the genome of a hyper-thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
                                                                                                                                                                                                                                                                                                                                          01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
387AA LONG HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                          058754;
                                                                       SEQUENCE
                                                                                                                 DNA Res. 5:55-76(1998).
EMBL; AP000004; BAA30141.1;
MEROPS; M40.002;
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NCBI_TaxID=53953;
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43058 MW;
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70.0%;
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07, Last sequence update)
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AMIDOHYDROLASE.
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2; Mismatches
                                    Score
Pred.
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd

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Perfect score:
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3. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*

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N-terminal sequenc Sequence of the to Sequence of the Ga E.coli HU849 Gal-G Pilin protein, Pap Bacterial P pilus Polypeptide sequen Human gastric canc Human 5' EST relat C glutamicum prote Human histone H2A.
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AAB78880 AAG17489 AAU34017 AAY70146 AAU36538	AAW99189 AAW99184 AAW55121 AAB34903 AAG34527 AAB53865 ABB50843 ABG15712 AAB78881 AAG78861	AAG61127 AAG06270 AAG58324 AAG61126 AAG58323 AAR75454 AAB853179 AAR75453 AAW88413 AAW88413	ABG17822 AAM00820 AAM42264 AAM00984 AAM00984 ABG21990 AAG61128 AAG6571 AAG58325
C. glutamicum SRT Arabidopsis thalia Staphylococcus aur Staphylococcus aur Staphylococcus aur	Alternatively spli Osf2/Cbfal native Streptococcus pneu Gene 1 human secre Arabidopsis thalia Human colon cancer Human secreted pro Novel human diagno C. glutamicum SRT C glutamicum prote		Novel human diagno Human bone marrow Human ORFX ORF2028 Human ORFX orF2028 Human bone marrow Novel human diagno Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia

ALIGNMENTS

A CCC RESULT 1 AAR03021 Receptor specific protein compsns. isolated from E.coli - useful for blood and tissue typing and for tissue staining Hull RA, Hull SI, Nowicki B; WPI; 1990-036830/05. 09-JUL-1987; 09-JUL-1987; 21-DEC-1989. US4882425-A. Escherichia coli. En; Dr; DrCMR; Pglobo; tissue receptor; blood typing N-terminal sequence of Pglobo receptor specific protein. 11-JUL-1990 (first entry) AAR03021; AAR03021 standard; protein; (BAYU) BAYLOR COLEGE OF M. 87US-0072197 87US-0U72197 24 A

Protein has antigenic specificity for blood and tissue surface antigens.

Claim 1; Page 18; 10pp; English.

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RESULT 2
AAP91911
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                                 RESULT 3
AAP50045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  May be used in blood and tissue typing for transfusion/transplantation, paternity testing, disease diagnosis and tissue staining.
                                                                                                                                                                                            An actual mol. wt. of 16.4kD can be calculated from the sequence. Fill-type fimbriae was purified from CH4 (02:K1:H-serotype) E. colisolated from the affected hearts of chickens with colibacillosis. The first 17 amino acids at the N-terminal are identical to the Fil subunit. A vaccine prepd. was prepared from Fil-type fimbriae which protected poultry from E.coli septicaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E.coli septicaemia; F11-type CH4 wild type E. coli strain
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                                                                                                                                                                                                                                                                            Fig 1; page 11; 14pp; English.
                                                                                                                                                                                                                                                                                                   antibodies against these
                                                                                                                                                                                                                                                                                                            Vaccine for protecting poultry against E.coli septicaemia contg. F11-type fimbriae or immunogenic sections, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence of fimbriae.
 AAP50045;
                       AAP50045 standard;
                                                                                                                                                                        Sequence
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|PQGQGKVT 12
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                                                                                                                            Conservative
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                      protein; 163 AA
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(02:K1:H-serotype)
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Pred. No. 2.2;
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RESULT 4
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AC AAP6
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                    Methods for the prodn. of vaccines using AAP50045 and each of the specified antigenic regions (see FT) are individually claimed. AAP50045 and its fragments are highly effective and specific in generating antibodies to urinary pathogens, and are obtainable practical amts. and in pure form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Region
                                                                                                                                                                                                                                                                                                                   Vaccines against urinary tract infections gal-gal pilus protein or fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia
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                                                                                                                                                                                                                                                                                                                                                                        O'Hanley P,
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                                                                                                                                                                                                                   Sequence
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 HU849; pilin; vaccine; urinary tract infection; ss
                    E.coli HU849
                                                             AAP60247;
                                                                                 AAP60247 standard; protein; 163
                                                                                                                                                                                                                                                                                                                                                                                           (STRD ) LELAND STANFORD JR UNIV.
                                         30-JUL-1991
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                                                                                                                                                     1 PQGQGKVT 8
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                     Gal-Gal pilus protein.
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/note= "isolated as a CNBr-HFBA III fragment"
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/note= "sequence corresponding to the tryptic
                                                                                                                                                                           100.0%; S
100.0%; F
tive 0;
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Pred. No. 2.2
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                                                  13-JUL-1999;
16-JUL-1999;
23-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccines containing this protein confer protection against urinary infections, so that the need for antibiotic therpy is avoided. The protein is from a specific type of pilus associated with most uropathogenic E. coli strains. The peptide fragments Pro(5)-Thr(12) and Ala(65)-Gly(75), each optionally having a Cys residue at one of their terminii, are separately claimed. Any protein whose amino acid sequence includes one of these fragments is suitable for use in a vaccine, esp. the CNBr-II fragment corresponding to amino acids 53-163 of HU849 pilin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New peptide(s) having 8 or 11 amino acid residues - useful with derivs. as conjugates in vaccines for conferring protection against urinary tract infections
                                                                                                                                                                                                                                                                                    AAB47081 standard;
         Hultgren
                                                                                                                                                              Escherichia coli.
                                                                                                                                                                                    Donor; pilus protein; pilin; adhesin; vaccine; urinary epithelia; urinary tract infection; enterobacteriaceae.
                                                                                                                                                                                                                   Pilin protein, PapA.
                                                                                                                                                                                                                                          08-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                               (MEDI-) MEDIMMUNE INC
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2000US-0184442.
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         Pinkner JS,
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          Sauer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunogenic complexes act by disrupting pilus-mediated attachment of E. coli to urinary epithelia and may prevent or retard the development of urinary tract infections. Vaccines containing the complexes are useful for preventing urinary tract disease in a human caused by the bacterium family enterobacteriaceae specifically Escherichia coli and may also be used in treating the disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adhesins, such as FimH are relatively conserved proteins among different species and strains of the strains, therefore vaccines incorporating the FimH antigen exhibit a broad spectrum of protection compared with current pilus-fiber based vaccines.
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                                                                                                                    WPI; 2001-226496/23.
                                                                                                                                               Hultgren
                                                                                                                                                                                                     11-AUG-1999;
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                                                                                                                                                                                                                                                                                  WO200110386-A2
                                                                                                                                                                                                                                                                                                             Bacteria.
                                                                                                                                                                                                                                                                                                                                     Antibacterial compound; Gram-negative bacterium; biofilm; disease treatment; bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                              Bacterial P pilus subunit PapK
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                                                                                          An isolated
                                                                                                                                                                       (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                       15-FEB-2001
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                                                                                                                                               SJ,
                                                               Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163
                                                                                          compound for inhibiting
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                                                                                                                                               Sauer
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                                                             144pp;
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Pred. No.
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The present invention provides antibacterial compounds which are able interfere with Gram-negative bacteria pilus formation and assembly, an pilus interaction with chaperone proteins. These are useful in the treatment of bacterial infection, and in the prevention of biofilm

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Best Local S
Matches 8
                                                                                                             reproductive-specific proteins are useful for diagnosing infertility which is a result of reduced sperm count, reduced sperm motility, malformed sperm or combinations of these. The sequences of the inventiare useful as markers for spermatogonial cells, for identifying genes proteins characteristic of male infertility, diagnosing or aiding in the diagnosis of infertility in men, and for contraception in which sperm production or sperm count is reduced or defetive sperm is produced. Antibodies to reproductive-specific proteins are useful for determining the presence of these proteins in a sample obtained from a man being assessed for infertility, for identifying the expression of genes in particular cell type or particular developmental stage, for studies of spermatogenesis, and for immunofluorescence of germ cells of the second of 
                      in Western blots for assessing the presence of the protein the antibody binds. The sequences of the invention are also useful for treating disorders of reduced sperm count, and for increasing sperm count and/or sperm activity. The nucleic acids of the invention are useful in gene
                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to the isolation of novel mammalian human reproductive-specific proteins (AAU07859-AAU07899), and the nucleic acids encoding them. The nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel reproduction-specific protein, useful for treating disorders reduced sperm count, enhancing/increasing sperm count and/or sperm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAS13663.
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12-JAN-2001; 2001US-0261557.
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  invention are useful in human reproduction-spec
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                                                                                                                                                                                                                          represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively.

AAB63732 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nu acids or anti-CAAP antibodies are useful for diagnosing and treating condition characterised by expression of an abnormal amount of a proceeding the protein of the protein of a procession condition characterised by expression of an abnormal amount of a procession condition characterised by expression of an abnormal amount of a procession condition characterised by expression of an abnormal amount of a procession condition characterised by expression of an abnormal amount of a procession condition characterised by expression of an abnormal amount of a procession condition characterised by expression of an abnormal amount of a procession condition characterised by expression of an abnormal amount of a procession condition characterised by expression of an abnormal amount of a procession condition characterised by expression of an abnormal amount of a procession condition characterised by expression of an abnormal amount of a procession condition characterised by expression condition characterised by expression of an abnormal amount of a procession condition characterised by expression characteristerised by expression characterised
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
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                                                                                                                                                                  Sequence
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99US-0153454.
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antigen; cytostatic;
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                                                                                                     DB
31;
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                                                                                                                                                                                                                          CAAP proteins, peptides, nucleic for diagnosing and treating a an abnormal amount of a protein,
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                                     RESULT 10
                                                                                                                                                                                                 CC sequences, corresponding to human secreted proteins. AAX6451 to CC AAX65438 represent the EST related proteins corresponding to AAX4265 to AAX63052. The 5' ESTs can be used for producing secreted human gene CC products. They can be used to identify and isolate 5' untranslated C regions (UTRs) and upstream regulatory regions which control the CC location, development stage, rate, and quantity of protein synthesis, as CC well as stability of mRNA. The ESTs are also useful as probes for CC well as stability of mRNA. The ESTs are also useful as probes for CC also be used in forensic procedures to identify individuals, or in CC diagnostic procedures to identify individuals, or in CC diagnostic procedures to identify individuals having genetic diseases resulting from abnormal gene expression. The products may also be used in gene therapy protocols. The nucleic acids encoding signal peptides can be used for directing extracellular secretion of a polypeptide or the CC insertion of a polypeptide into a membrane, or importing a polypeptide or the control artists of them conditions. Secreted proteins have CC therapeutic value, and the identification of new secreted proteins is CC callable. AAX42264 to AAX42264 and AAX46640 represent
                                                                                                                     Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                    AAZ42265 to AAZ43075 represent novel 5' expressed sequence tag (EST) sequences, corresponding to human secreted proteins. AAY64651 to
             AAG92121 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 777; 837pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel secreted protein 5' expressed diagnostic, forensic, gene therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-APR-1998;
28-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy; chromosome mapping; upstream regulatory
forensic; location; development; protein synthesis; st
                                                                       26
                                                                                               1 PQGQGKVT 8
                                                                       PQGSGRIT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5' EST;
                                                                                                                      Similarity
5; Conser
                                                                                                                                                                                           used
                                                                                                                                                                     123
                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                     A
                                                                                                                                                                                          in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expressed sequence tag; secreted protein; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0057719
98US-0069047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-IB00712.
             Protein;
                                                                                                                               79.1%;
62.5%;
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                                                                                                                      ν,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123
                                                                                                                                Score 34; DB Pred. No. 76;
                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence tag sequences used in and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Giordano
                                                                                                                                                                                       of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŗ,
                                                                                                                   1;
                                                                                                                                           Length 123;
                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              stability;
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                                                                                                                   Gaps
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 Ωy
                                                                                                                                                                                                                                                               AAB73702
                                                                                                                                                                    밁
                                                                                                                                RESULT 11
                                                                                                                                                                                                               Query Match
Best Local S
Matches 5
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakagawa
Tateishi
Histone H2A.21; human; his
malignant tumour; cancer;
                                  Human histone H2A.21.
                                                                                                                                                                                                                                                              Sequence
                                                         11-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP1108790-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG92121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-DEC-2000;
                                                                                                                                                                                       PQGQGKVT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'z 'o
                                                                                                                                                                                                                                                               143
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                             AAB73702 standard; Protein; 194 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coryneform bacterium; amino acid synthesis; vitamin; organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C glutamicum protein fragment SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                            81 PDGQGRIT 88
                                                                                                                                                                                                                                                                                                                                                                          Similarity
5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO: 5875; 246pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mizoguchi H,
Senoh A, Ik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99JP-0377484.
2000JP-0159162.
2000JP-0280988.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB
Pred. No. 88;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             2;
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                                                                                                                                                                                                                                                                                                                                                                                                                               22;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Length 143;
                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yokoi H;
                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                          Gaps
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histone H2A.1 homologue; recombinant production; er; blood disease; HIV infection;

0;

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RESULT 12
ABG17822
   This sequence represents human histone H2A.21. The protein has a complecular weight of 21 kD, and has 98% identity and 100% homology with human histone H2A.1 (GenBank accession number M60752) over an 84 camino acid stretch. The invention relates to human histone H2A.21 (ARB73702), nucleic acids encoding it (ARB24271), and a method for the recombinant production of human histone H2A.21. The present invention additionally discloses an antibody which specifically binds to human histone H2A.21. The present invention additionally discloses an antibody which specifically binds to human can histone H2A.21. The present invention may be used for treating a variety of diseases, such as malignant tumours, blood diseases, HIV (human immunodeficiency virus) infection. Immune disorders and inflammatory conditions. The protein may also be used to screen for modulators of its activity or for peptide fingerprinting identification. The polynucleotide can be used as a primer for nucleic acid amplification reaction or as a probe for hybridisation reactions, or in producing gene chips or microarrays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                   latches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human histone H2A.21 for diagnosing and treating malignant tumor, hemopathy, human immunodeficiency virus (HIV) infection, immunological diseases and inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human immunodeficiency virus; immune disorder; inflammatory condition; cytostatic; anti-HIV; antiinflammatory; immunomodulator.
30-MAR-2001; 2001WO-US08631.
                                  11-OCT-2001
                                                                 WO200175067-A2
                                                                                                                                                                                  Novel human
                                                                                                                                                                                                                   18-FEB-2002
                                                                                                                                                                                                                                                                                 ABG17822 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAH24271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-355930/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200138522-A1
                                                                                                                                food supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BIOR-) BIOROAD GENE DEV LTD SHANGHAI.
                                                                                                                                                                                                                                                                                                                                                                  125 PQGQGQV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 1 PQGQGKV 7
                                                                                                                               chromosome mapping; gene mapping; gene therapy; forensic;
upplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 AA
                                                                                                                                                                               diagnostic protein #17813
                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                               79.1%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; D
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
1.2e+02;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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RESULT 13
AAM00820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for identifying expressed genes. (I) is useful in gene therapy techniques (C) to restore normal activity of (II) or to treat disease states involving (C) (II), (II) is useful for generating antibodies against it, detecting or cyantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical considers involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC anino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention. CC diagnostic amino acid sequences of the invention. CC diagnostic amino acid sequences of the invention of the printed control of the sequence data for this patent did not appear in the printed control of the polypeptication, but was obtained in electronic format directly from WIPO at the printed control of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags
                                                                                                                                                                                        antiviral; antibacterial; antifungal; anti-HIV; haemostatic;
immunosuppressive; gene therapy; cytokine cell proliferation;
cell differentiation modulator; immune disorder; infection; c
                                                                                                                                                                                                                                   Human; bone marrow; antiinflammatory; cytostatic; neuroprotective;
antiviral; antibacterial; antifungal; anti-HIV; haemostatic;
                                                                                                                                                                                                                                                                                                             Human bone marrow protein, SEQ ID NO: 183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID No 48181; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                               Homo sapiens
                                                                                                                                                                  human immunodeficiency
                                                                                                                                                                                                                                                                                                                                                               01-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                AAM00820
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM00820 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide (II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-639362/73
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 PQGQGK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POGQGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                486 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu C,
                                                                                                                                                                                                                                                                                                                                                               (first entry)
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2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34;
Pred. No.

    is useful as hybridisation probes,

                                                                                                                                                                  HIV; autoimmune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 486;
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                                                                                                                                                                                        cancer;
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WO200153453-A2

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RESULT 14
AAB42264
      Best
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25-APR-2000;
09-JUL-2000;
Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunosuppressant; cardiant; immunosuppressant; cardiant; immunosuppressant; cardiant; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antifuematic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. haemophilia), inhibition of tumour cell proliferation suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease. Detection of the presen or increased expression of the polynucleotide or the protein it encodes is useful for the diagnosts and/or prognosis of one or more types of cancer. The polynucleotide and polypeptide can be used as nutritional sources or supplements and in the screening of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          by a bone marrow-expressed polynucleotide. The polynucleotide and the polypeptide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders may be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal infertion or may result from
                                                                                                                                                                                                                                         08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ford
                                                                                                                                                                                                        Human ORFX ORF2028 polypeptide sequence SEQ ID NO:4056.
                                                                                                                                                                                                                                                                                                       AAB42264 standard; Protein; 2434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chemical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 10; Page 338-339; 648pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel bone-marrow-expressed polynucleotides and polypeptides, for treating e.g. cancer and immune deficiency disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-NOV-2000;
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03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                   PQGEGTVT 284
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DB; AAH89939.
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, Zhou
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2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0250583.
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2000US-0598042.
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Werhman T, Xu C,
    Drmanac RT;
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75.0%;
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Pred.
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5.7e+02;
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Yang Y, 2
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                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-1999;
02-APR-1999;
05-APR-1999;
                                                                                                                                                                                                            1119
                                                                                                                                                                                                                                                                                                                                                                                                    vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
                                                                                              AAM00984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive.
                              Human bone marrow protein,
                                                              01-OCT-2001
                                                                                                                            AAM00984 standard; Protein;
                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11;
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DB; AAC76473.
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99US-0127636.
99US-0127728.
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75.0%;
                              SEQ ID NO:
                                                                                                                                                                                                                                                                       Score 34; DB Pred. No. 1.6e 1; Mismatches
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                                485.
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1.6e+03;
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Human; bone marrow; antiinflammatory; cytostatic;

neuroprotective;

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Search completed: October 28, Job time: 24.3158 secs
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                                                                                                                                                                                                                                   The present sequence is one of 251 novel human polypeptides encoded CC by a bone marrow-expressed polynucleotide. The polynucleotide and the polypeptide encoded by it are useful in the treatment of various commune deficiencies and disorders. The deficiencies and disorders may be caused by a viral (e.g. HIV), bacterial or fungal confection, or may result from an autoimmune disorder, a coaquiation, cc suppression of an inflammatory response or treatment of a nervous cystem disorder such as Alzheimer's disease. Detection of the presence or increased expression of the polynucleotide or the protein it encodes is useful for the diagnosis and/or prognosis of one or more types of cancer. The polynucleotide and polypeptide can be used as nutritional sources or supplements and in the screening of chemical compounds as potential drugs.
                                                                                                                                     Query Match 79.1%;
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-055317.
09-JUL-2000; 2000US-0598042.
19-UL-2000; 2000US-0620312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0662191.
19-CCT-2000; 2000US-0693036.
30-NOV-2000; 2000US-0250583.
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| 1279 PQGEGTVT 1286
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Ren F, Wang J, Werhman T, Xu
Zhao QA, Zhou P, Drmanac RT;
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immunosuppressive; gene therapy; cytokine cell proliferation;
cell differentiation modulator; immune disorder; infection; cancer;
human immunodeficiency virus; HIV; autoimmune disorder; haemophilia.
                                                                                                                                                                                                        Sequence
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N-PSDB; AAH90103.
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                   2002, 17:22:38
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Pred. No. 1.7e+03;
1; Mismatches 1
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Listing first 45 summaries
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Perfect score:
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   protein search, using sw model
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/packfiles1.pep:*
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  PQGQGKVT 8
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Copyright (c) 1993 - 2002 Compugen Ltd
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  BB
        US-09-100-193-3
US-08-961-083-126
US-08-961-083-136
US-08-961-083-136
US-08-961-083-136
US-08-481-985B-70
US-08-481-985B-70
US-08-910-927B-1
US-09-270-270-1
US-09-270-270-1
US-08-910-927B-1
US-09-270-270-1
US-08-76-136-1
US-08-772-440-32
US-08-772-440-14
US-08-772-440-15
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        Sequence 3, Appli
Sequence 118, App
Sequence 118, App
Sequence 136, App
Sequence 6, Appli
Sequence 6, Appli
Sequence 70, Appl
Sequence 70, Appl
Sequence 1, Appli
Sequence 2, Appli
Sequence 16, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 11, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 10, Appl
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Sequence
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PQGQSQIT 278 PQGQGKVT

Query Matc Best Local Matches	RESULT 1 US-09-100-193-3 Sequence 3, Applicat patent No. 6153729 GENERAL INFORMATION APPLICANT: GATY TITLE OF INVENTION NUMBER OF SEQUENC CORRESPONDENCE AD ADDRESSEE: LAH STREET: 28 Sta CITY: Boston STATE: Massach COUNTRY: USA ZIP: 02109 COMPUTER READABLE MEDIUM TYPE: FACOMPUTER READABLE COMPUTER: 1BM OPERATING SYSTE COMPUTER: 1ENT APPLICATION NUM FILING DATE: CLASSIFICATION NUM PRICIATION NUM APPLICATION NUM RECITATION NUM RECITATION NUM RECITATION NUM RECITATION NUM RECITATION NUM RECITATION FOR SEQUENCE CHARACTE (617) INFORMATION FOR SEQUENCE CHARACTE LENGTH: 513 am TYPE: amino ac TOPOLOGY: 11ne MALEULE TYPE: amino ac TOPOLOGY: 11ne MALEULE TYPE: pholesule MOLECULE TYPE: pholesule MOLECULE TYPE: pholesule Molecule Type: pholesule frackent Type: pholesul		22 22 23 23 23 23 23 23 23 24 24 24 25 26 26 27 28 28 28 28 28 28 28 28 28 28 28 28 28
	1 1 00-193-3 nce 3, Applic to No. 6153729 RAL INFORMATI PLICANT: Gar TLE OF INVENT MBER OF SEQUE RRESPONDENCE ADDRESSEE: 128 5 CITY: BOSTON STATE: Massa COUNTRY: USA MEDIUM TYPE: COMPUTER READAR MEDIUM TYPE: COMPUTER READAR MEDIUM TYPE: CASSIFICATION N FILING DATE: CLASSIFICATION N FILING DATE: CLASSIFICATION PILING DATE: CLASSIFICATION REFERENCATION REFERENCATION REFERENCATION REGISTRATION R		$\begin{smallmatrix} 0&0&0&0&0&0&0&0&0&0&0&0&0&0&0&0&0&0&0&$
n Similarity 5; Conserva	DOUBLE VO HENNON MODENT C CHUREN. E		67.4 67.4 67.4 67.4 67.4 67.4 67.4 65.1 65.1 65.1 65.1 65.1 65.1 65.1
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å. å.			414544445500004440
Score 32; DB 4; Pred. No. 1.8e+02; 2; Mismatches 1	al. MATRIX TARGETING TELD TELD MS-DOS e #1.0, Version #1 //100,193 //100,193 UMM-024 N:	ALIGNMENTS	US-09-268-364-2 US-08-594-808B-7 US-08-971-188-8 PCT-US91-08442-2 US-09-460-145-4 US-09-460-145-4 US-09-88-27-208-3 US-09-498-809-3 US-09-498-809-3 US-09-494-10257A-51 PCT-US94-10257A-52 PCT-US94-10257A-62 PCT-US94-10257A-80 US-08-488-161-30 US-08-488-161-30 US-08-488-161-30 US-08-488-161-30 US-08-488-161-30 US-08-973-685-30 US-09-063-950-9 US-09-063-950-9 US-09-091-219-6 US-09-091-219-6
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RESULT 3
US-08-961-083-118
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US-08-961-083-120
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APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Choi e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 120:
SEQUENCE CHARACTERISTICS:
LENGTH: 522 amino acids
       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                  TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                      131 QGQGKVS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: Sir
TOPOLOGY: linear
OPERATING SYSTEM:
                                                                                        COUNTRY:
                                                                                                                          STREET: 9410 Key
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity es 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                        2 QGQGKVT 8
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                                                                       20850
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                                                                                                           Maryland
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                                                                                                                                             9410 Key West Avenue
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                                                                                                                                                                                                                                        Choi et. al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                            Human Genome Sciences, Inc.
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85.78;
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MSDOS version 6.2
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    Mismatches

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Pred. No. 1.8e+02;
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; LENGTH: 1040 amino
; TYPE: amino acid
; STRANDEDNESS: sinc
; TOPOLOGY: linear
; MOLECULE TYPE: prote
US-08-961-083-118
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US-08-961-083-136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 118: SEQUENCE CHARACTERISTICS: LENGTH: 1040 amino acids
                                                                                   TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
                                                SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
                                                                                                                                    REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Choi et. al. TITLE OF INVENTION: Str
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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CLASSIFICATION: 435
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les 6; Conserv
                                                                                                                     TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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TOPOLOGY:
              STRANDEDNESS:
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                                  amino acid
                                                                                                                                                                                      Brookes, A. Anders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9410 Key West Avenue
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85.7%;
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                                                                                     136:
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    Mismatches

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Pred. No. 3.7e+02;
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; MOLECULE TYPE: US-08-961-083-136
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                                                                                                                                                                  RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: A-59
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEPAX: (415) 494-8771
TELEX: 210 277299
INFORMATION FOR SEQ ID NO: 6:
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Best Local Similarity
Matches 5; Conserv
                                                                                                                    Sequence 6, Application US/08818823 Patent No. 5708158
                                                                                                                                                                                                                                                                          Matches
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Best Local :
                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HOEY, Tinothy
TITLE OF INVENTION: NUCLEAR FACTORS AND BINDING
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                         CORRESPONDENCE ADDRESS
                                                      APPLICANT: HOEY, Timothy
TITLE OF INVENTION: NUCLEAR FACTORS
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                       Local Similarity
nes 6; Conserv
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              STREET:
                                                                                                                                                                                                                                1 POGOGKV 7
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   amino acid

OGY: linear
San Francisco
           E: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT 4 Embarcadero Center, Suite 3400
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85.7%;
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83.3%;
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Pred. No. 4.
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Pred. No. 1.3e+02;
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                                                                       AND BINDING
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..9e+02;
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US-08-484-905-70
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Best Local S
Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 70,
              APPLICATION NUMBER: US/08/484,905
FILING DATE: 07-UNE-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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TELEX: 210 277299
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS-MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: An Altered Major Histocompatibility
TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
TITLE OF INVENTION: Determinant
TITLE OF INVENTION: Determinant
TITLE OF INVENTION: Determinant
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: UFILING DATE: 14-MAR-1 CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/39
FILING DATE: 02-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
PRIOR APPLICATION DATA:
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nes 6; Conserv
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.1%;
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Pred. No. 4.9e+02;
0; Mismatches 1
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APPLICATION NUMBER: FILING DATE: 15-NOV CLASSIFICATION: 530

15-NOV-1991

US 07/792,473

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; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-484-905-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-481-985B-70
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                                                                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/481,985B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UDMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 435
PRIOR APPLICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 70,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
           TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     st Local Similarity
tches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: POTTEY, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202,408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1000
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 311 amino acids
                                                                                      REFERENCE/DOCKET NUMBER: 03
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 148 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: D.C.
STATE: D.C.
STP: 20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Mottez,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193 PRSEGKVT 200
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                        NAME: Meyers, Kenneth J. REGISTRATION NUMBER: 25,146
                                                                     TELEPHONE:
LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 POGOGKVT 8
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1300 I Street, N.W., Suite 700
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Kourilsky, Phillipe
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                                                                     202-408-4000
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Pred. No. 2.6e+02;
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Query Match
Best Local Similarity
"~+~hes 5; Conserva
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                                                                           ; MOLECULE TYPE: US-08-370-476-70
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Best Local Similarity b2...
5; Conservative
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Patent No. 6153408
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                                                                                                                                                                    TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                      SEQUENCE CHARACTERISTICS
LENGTH: 311 amino acid
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
PRIOR APPLICATION UNMBER: US 07/792,473
FILING DATE: 15-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 0 FILING DATE: 06-JUN-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/370,476
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,575
FILING DATE: 07-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                  FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: D.C.
STATE: D.C.
FTP: 20005-3315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193 PRSEGKVT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1300 I STREET: Washington
                                                                                                                                                                                                                                    NAME: Meyers, Kenneth J
REGISTRATION NUMBER: 25,
REFERENCE/DOCKET NUMBER:
                                                                                                       TOPOLOGY:
                                                                                                                            TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 PQGQGKVT 8
                                                                                                                           amino acid
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                                                                                                                                         311 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Casrouge, Armanda
VENTION: Altered Major Histocompatibility Complex
                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Abastado, Jean-Pierre
Kourilsky, Phillipe
Lone, Yu-Chun
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                                                                                      peptide
                           69.8%;
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              Score 30; DB
Pred. No. 2.6e
2; Mismatches
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Pred. No. 2.6e+02;
2; Mismatches 1
                                6e+02
                                            Length 311;
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                Indels
                0;
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                Gaps
                0;
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193 PRSEGKVT 200

PQGQGKVT 8

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RESULT 10
US-08-828-242-1
                                                                                                                                                     RESULT 11
US-08-910-927B-1
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                                                                                                       Sequence 1, Application US/08910927B Patent No. 5976801 GENERAL INFORMATION:
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Patent No. 5871970
                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                            APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/8: FILING DATE: Filed Herewith CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hillman, Jennifer L.
APPLICANT: GO11, Surya K.
TITLE OF INVENTION: NOVEL CALCIUM-BINDING
TITLE OF INVENTION: PROTEIN
                                                                        APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: B1111ngs, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                Local Similarity
les 5; Conserv
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ZIP: 94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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                                                                                                                                                                                                                                                 1 PQGQGKV 7
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                         Shah, Purvi
                                                        Lal, Preeti
                                           Corley, Neil C.
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                        CONUTUT01
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                                                                                                                                                                                                                                                                                                                                                                                                       linear
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 HUMAN RETICULOCALBIN ISOFORMS
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Pred. No. 2.7e+02;
1; Mismatches 1;
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RESULT 12
US-09-206-499-1
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                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09206499 Patent No. 6194385
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Matches 5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL CALCI
TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                 SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: RATRN
CLONE: 922578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION UNBER: US/08/910,927B FILING DATE: Hereewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 3174 POI
CITY: Palo Alto
STATE: CA
                                                 COMPUTER: IBM COR
OPERATING SYSTEM:
                                                                                                                        COUNTRY:
                                                                                                                                                    STATE:
                                                                                                                                                              STREET: 3174 POI
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                 28 PHGQGRV 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                ADDRESSEE:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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 US/09/206,499
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Pred. No. 2.7e+02;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/8:
FILING DATE: 03/31/1997
ATTORNEY/AGENT INFORMATION:

08/828,242

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INFORMATION FOR SEQ ID NO: 1:
             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acid
                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                        REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 PHGQGRV 34
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CITY: Palo Alto
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les 5; Conserv
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CLONE: 2509570
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                                                                           TELEFAX:
                                                                                                                                       NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/270,270
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: 328 amino acids
amino acid
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Shah, Purvi
                                                                            650-845-4166
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Hillman, Jennifer
Lal, Preeti
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71.4%;
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Pred. No. 2.7e+02;
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RESULT 15
US-08-476-509B-4
; Sequence 4, Application US/08476509B
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/348
FILING DATE: 01-DEC-194
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26.742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 11-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: RATRNOTO2
CLONE: 922578
                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                   LENGTH: 454 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: A SH2 DOMAIN ASSOCIATED PROTEIN, A TITLE OF INVENTION: SIGNALLING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTIC TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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CORRESPONDENCE ADDRESS:
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CITY: Hackensack
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71.4%;
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83.3%;
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                                                                                                                                                   Score 30; DB 3;
Pred. No. 3.8e+02;
1; Mismatches 0
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Pred. No. 2.7e+02;
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GENERAL INFORMATION:
APPLICANT: PERE JORN
APPLICANT: SIGNALING DOMAIN ASSOCIATED PROTEIN, A
APPLICANT: PERET JORN
APPLICANT: PERET JORN
APPLICANT: HERRY. CHEN
TITLE OF INVENTION: SIGNALING DOMAIN, MICLEIC ACIDS ENCODING THE
TITLE OF INVENTION: SIGNALING DOMAIN, AND DIAGNOSTIC AND THERAPEUTICUSES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: All Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUTRY: USA
CONTRY: USA
CONTRY: USA
CONTRY: USA
CONTRY: USA
CONTRY: HEREOF
NUMBER: OF SOLIT
CONTRYER READALE FORM:
MEDIUM TYPE: Floppy disk
CONTRYE: USA
CONTRY: USA
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OM protein - protein search, using sw model Searched: Scoring table: Sequence: Perfect score: al number of hits satisfying chosen parameters: October 28, 2002, 17:21:20 ; Search time 11.7895 Seconds (without alignments) 65.203 Million cell updates/sec 283138 seqs, BLOSUM62 US-09-833-079-1 43 Gapop 10.0 , 1 PQGQGKVT 8 GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compus 96089334 residues Gapext 0.5 Compugen Ltd

Minimum DB Maximum DB seq length: 0 length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database PIR_71:* pir1:*
pir2:*
pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5)	ω	N	-		Result
32	32	32	32	32	32	32	32	32	32	32	32	32	33	33	33		33		34	34	35	35	35	35	40	43	43	43		
74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	76.7	76.7	76.7	76.7	76.7	79.1	79.1	79.1	81.4	81.4	81.4	81.4	93.0	100.0	100.0	100.0	Maccii	
513	433	412	328	300	277	277	243	231	210	199	185	176	1119	681	469	229	195	745	136	134	613	469	187	187	182	188	185	161	- enden	
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A48233	T09619	S28423	AH0034	D87609	T43138	T38987	T46461	E81235	S36394	A90344	D84456	AG0336	T50995	E81815	G70690	B90513	B75273	B70017	T09477	T46114	T42671	S76891	C43597	YQECKS	141204	YQECF2	YQECPP	S25206	15	;
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45	44	43	42	41	40	39	38	37	36	35	34	ω u	32	31	30
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72.1	72.1	72.1	72.1	72.1	72.1	72.1	72.1	72.1	72.1	74.4	74.4	74.4	74.4	74.4	74.4
299	299	255	249	216	205	180	174	172	38	2938	1856	1749	899	897	894
N	N	Ŋ	N	Ŋ	N	N	Н	N	N	N	N	2	N	N	1
D98109	F95244	C71169	A87520	T03637	C89814	A05072	A31096	G70234	T11763	T30249	C95008	S75071	T11578	S02032	FAHUA2
UTPglucose-1-pho	UTP-glucose-1-phos	probable flagellin	hypothetical prote		hypothetical prote	RNA-directed DNA p	fimbrial protein p	conserved hypothet	acetyl-CoA carboxy	cell proliferation	immunoglobulin Al	hypothetical prote	probable lipoxygen	alpha-actinin 2, s	alpha-actinin 2 -

ALIGNMENTS

A;Gene: prsA C;Superfamily: F7-2 fimbrial protein A; Experimental source: strain 1442 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199C;Species: Escherichia coli
C;Date: 17-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 26-Aug-1999 A;Cross-references: EMBL:X62157; NID:g42515; PIDN:CAA44083.1; PID:g42516 A;Experimental source: strain 1442 A; Molecule type: DNA A; Residues: 1-161 <MAR> A; Title: Horizontal gene transfer of the Escherichia coli pap and prs pili operons as A; Reference number: S25205; MUID:93023852 R; Marklund, B.I.; Tennent, J.M.; G Mol. Microbiol. 6, 2225-2242, 1992 C; Genetics: A; Status: nucleic acid sequence not shown; translation not shown A; Accession: S25206 R; Marklund, B.I.; C; Accession: prsA protein -Escherichia coli (strain 1442) (fragment) Garcia, E.; Hamers, A.; Baga, M.; Lindberg, F.; Gaas Length 161;

δã 밁 Query Match Best Local 9 Matches 6 PQGQGKVT 13 1 PQGQGKVT 8 Similarity 8; Conserv 100.0%; ilarity 100.0%; Conservative 0 0 Score 43; DB 2; Pred. No. 0.44; Mismatches 0 Indels 0; Gaps

0;

fimbrial protein papA precursor - Escherichia coli N;Alternate names: pap pili C;Species: Escherichia coli

C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Jul-1999 C;Accession: A23221; S25216; A05229; S16395 R;Baga, M.; Normark, S; Hardy, J; O'Hanley, P.; Lark, D.; Olsson, O.; Schoolnik, G. J; Bacteriol. 157, 330-333, 1984 P; Bacteriol. 157, 330-333, 1984 P; Bacteriol. 157, 30-333, 1984 P; Bacteriol. 15

A; Molecule type: DNA A; Residues: 1-185 <BAG>

A;Cross-references: GB:X03391; GB:K01176; GB:X03392; NID:g42309; PIDN:CAA27126.1; PID R;Marklund, B.I.; Tennent, J.M.; Garcia, E.; Hamers, A.; Baga, M.; Lindberg, F.; Gaas Mol. Microbiol. 6, 2225-2242, 1992
A;Title: Horizontal gene transfer of the Escherichia coli pap and prs pili operons as A;Reference number: S25205; MUID:93023852
A;Accession: S25216

A; Molecule type: DNA A; Residues: 1-185 <MA2>

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A;Cross-references: EMBL:X61239; NID:g42290; A;Experimental source: strain J96 C;Genetics: A;Gene: papA C;Superfamily: F7-2 fimbrial protein C;Keywords: fimbria F;1-22/Domain: signal sequence #status predic F;23-185/Product: fimbrial protein papA #stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Description: one of the fimbrial proteins involved in ubunits into fimbriae, or regulation of phase variation C.Superfamily: F7-2 fimbrial protein sywords: fimbria; mannose-resistant hemagglutination 21/Domain: signal sequence #status prodicted
                                                                        R;Maiti, S.N.; DesGroseillers, L.; Fairbrother, J.M.; Harel, J. Microb. Pathog. 16, 15-25, 1994
A;Title: Analysis of genes coding for the major and minor fimbrial subunits
                                                                                                                              A-minor fimbrial protein - Escherichia coli
C;Species: Escherichia coli
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
C;Accession: I41204; A44853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene 32, 83-90, 1984
A;Title: Nucleotide sequence
A;Reference number: A03496; M
A;Accession: A03496
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                A; Reference number: I41201; MUID: A; Accession: I41204
A; Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Infect. Immun. 59, 3849-3858, 1991
A;Title: DNA sequences of three papA genes from uropathogenic Escherichia coli strains:
A;Reference number: A43597; MUID:92040048
A;Accession: B43597
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A; Residues: 1-188 < VI
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A; Molecule type:
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A;Residues: 1-188 <DEN>
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;Function:
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;Date: 28 Feb-1986 #sequence_revision
;Accession: A03496; B43597
;Van Die, I.; Bergmans, H.
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88/Product: F7-2 fimbrial protein
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8; Conserv
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A;Cross-references: GB:L07420; NID:g1228096; PIDN:AAA92574.1; PID:g452584 R;Harel, J.; Forget, C.; Saint-Amand, J.; Daigle, F.; Dubreuil, D.; Jacquu J.; Gen. Microbiol. 138, 1495-1502, 1992 A;Tile: Molecular cloning of a determinant coding for fimbrial antigen F: A;Reference number: A44853; MUID:92381496 A;Contents: 4787, porcine wild-type A;Accession: A44853
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A;Molecule type: protein
A;Residues: 22-30,'1',32-35
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C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988
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                                                      A;Molecule type: DNA
A;Residues: 1-187 <DEN>
A;Residues: 1-187 <DEN>
A;Cross-references: GB:M68061; NID:g147072; PIDN:AAA24279.1; PID:g147073
C;Superfamily: F7-2 fimbrial protein
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C;Accession: C43597
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C; Species: Escherichia coli
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A; Residues: 1-187 < RHE>
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Eur. J. Biochem. 151, 573-577, 1985
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Infect. Immun. 59, 3849-3858,
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L; Mismatches
                                Score 35;
                  Pred. No. 19;
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hypothetical protein DKFZp434I1117.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
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A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
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A; Accession: T42671
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R; Bloecker, H.; Boe
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C; Superfamily:
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R; Kaneko, T.; Sato,
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A; Experimental source: adult test
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;Accession: S76891
Status: nucleic acid sequence not shown;
tolecule type: DNA
Residues: 1-469 <KANN
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K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada,
IA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                           Status: preliminary olecule type: mRNA esidues: 1-613 <AAA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: EMBL:D90917;
                                                                                                                                                                         417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  403
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                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                     1 PQGQGKV 7
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                                                                                                                                                                       PQGQGRV 423
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Synechocystis hypothetical protein sll0443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                              adult testis; clone DKFZp434I1117
                                                                                                                                                                                                                                                  81.4%;
85.7%;
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85.7%;
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was submitted
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                                                                                                                                                                                                                                   1;
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                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                   Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Asamizu,
lada, T.;
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                              R.; Weichselgartner,
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Yamada, M.; Yasuda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PID:g16538:
1996
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R;Murphy, L. submitted to the EMBL Data Library, January 1998 A:Reference number: Z16683
                                                                                                                                                                                                                                                                                                           hypothetical protein - human
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence
                                                                                                                                                                                                                                                                                                                                                         RESULT
T09477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 3
A;Introns: 58/3
A;Introns: 58/3
A;Note: T77B3.70
C;Superfamily: Arabidopsis thaliana hypothetical protein T21C14.30
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A; Status: prelimina
A; Molecule type: DN
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A;Residues: 1-134 <NYA>
A;Cross-references: EMBL:AL137079
A;Experimental source: cultivar Columbia; BAC clone T27B3
                                                                                                                     A; Introns: 27/3;
                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-136 <MUR>
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                                                                                                                                   A; Map position: 12
                                                                                                                                                A; Gene: 15E1.2
                                                                                                                                                             C; Genetics:
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Best Local Similarity
Matches 6; Conserv
                                                          Matches
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                                                          Local Similarity hes 5; Conserv
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26
                             1 PQGQGKVT 8
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                                                                                                                                                                                                                    preliminary; translated from GB/EMBL/DDBJ
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 PQGSGRIT
                                                                                                                   85/2;
                                                          Conservative
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                                                                                                                                                                                                                                                                                                              #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
                                                                                                                                                                              EMBL:AL021546; NID:e1248287; PID:e1248290
                                                                                                                     120/1
                                                                        79.1%;
62.5%;
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85.7%;
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                                                          2;
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Pred. No.
                                                                          Score 34;
Pred. No.
                                                          Mismatches
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21;
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RESULT 11

B70017

probable oxidoreductase (EC 1.-.-) yurC [similarity] - Bacillus subtilis
C;Species: D5-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
C;Accession: B70017
C;Accession: B70017
R;Kunst, F: Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C;Baron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galizci, A.; Galizci, A.; Galicci, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mal
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Accession: B70017
A;Scatus: nucleic acid sequence not shown; translation not shown

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A; Status, r--
A; Molecule type: DNA
A; Residues: 1-195 < WHI>
A; Cross-references: GB: AE002074;
A; Cross-teferences: Strain R1
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R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E;
, M.; Shen, M.; Vanathevan, J.J.; Lam, P.; McDonald, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacter A;Referrence number: A75250; MUID:20036896
A;Accession: B75273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene:
C;Superf
C;Keywor
                                                                                                                                                                                                R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; (Nucletc Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: B90513
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-745 <KUN>
A; Cross-references: GB: 299120;
A; Experimental source: strain 1
C; Genetics:
                                                                                                             A;Cross-references: GB:AL445566; 1A;Experimental source: strain UAB C;Genetics:
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C; Superfamily: Deinococcus radiodurans hypothetical
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A; Residues: 1-229 < KUR>
                                                                                                                                                                                                                                                                                                                                                                     50S ribosomal protein L1 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
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Best Local S
Matches 6
                                                                         Gene: MYPU_0100;
Genetic code: S
                                                                                                                                                                                                                                                                                                                               Species: Mycoplasma pulmonis;Date: 24-May-2001 #text_change 03-Aug-2001;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
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Species: Deinococcus radiodurans
Dec-1999 #sequence_revision 03-Dec-1999 #text_change 26-May-2000
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;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                 Accession: B90513
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Best Local
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                                                       Superfamily:
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 Similarity
                                                     Escherichia coli ribosomal protein
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75.0%;
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75.0%;
76.7%;
75.0%;
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                                                                                                                              PID:g14089423; PIDN:CAC13183.1; GSPDB:GN00153
B CTIP
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 Score
Pred.
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Pred. No. 48;
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Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein DR2446
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                   Length 229;
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                                                                                                                                                                                                                                                            pathogen Mycoplasma
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A;Reference number: A81775; MUID:20222556
A;Accession: E81815
                                                                                                                                                                                                                                                                                                      R; Parkhill, J.; Achtman, M.; James, Holroyd, S.; Jagels, K.; Leather, Nature 404, 502-506, 2000
                                                                                                                                                                                                                                                                                                                                                      probable transposase NMA1882 [imported] - Neisseria meningitidis (strain Z2491 serogr
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: E81815
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A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.;
A; Title: Deciphering the biology of Mycobacterium
A; Reference number: A70500; MUID:98295987
A; Accession: G70690
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A; Residues: 1-681 < PAR>
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A; Residues: 1-469 <COL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein Rv2812 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                   A; Experimental source:
                                                                                                                                                                                      A;Cross-references: GB:AL162757;
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1 rattus norv
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1 synechocyst
1 caenorhabdi
1 deinococcus
7 bacillus su
8 haloarcula
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5 synechocyst
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RESULT 2
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POGOGKVT

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0; Gaps	h 100.0%; Score 43; DB 1; Length 161; Similarity 100.0%; Pred. No. 0.17; 8; Conservative 0; Mismatches 0; Indels GQGKVT 8	Query Match Best Local Matches Qy 1 PQG
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Collaboration Citions on its in no way for commercial b.ch/announce/	ss-PROT entry is copyright. It is produced through a the Swiss Institute of Bioinformatics and the EME ean Bioinformatics Institute. There are no restrinon-profit institutions as long as its content is and this statement is not removed. Usage by and requires a license agreement (See http://www.isb-sin.email to license@isb-sib.ch).	This between the use modified entire
· x	propercies: ; robiol. 6:225-2242(1992). TION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS R TION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS R THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5 METERS AND NUMBERING 100-300 PER CELL, ENABLE BACTE BILDIAR THE EPITHELIUM OF SPECIFIC HOST ORGANS. ELLULAR LOCATION: Secreted. LARITY: BELONGS TO THE FIMA/PAPA FAMILY OF FIMBRIA P	RI MOL. Mic. RL MOL. Mic. CC -I- FUNC CC FROM CC MICR CC COLO CC -I- SUBC CC -I- SIMI
ດ ທ	FROM N.A. 42; 3023852; PubMed=1357526; BI., Tennent J.M., Garcia E., Hamers A., Baga M., F., Gaastra W., Normark S.; al gene transfer of the Escherichia coli pap and pr a mechanism for the development of tissue-specifi	[1] SEQUE STRAJ MEDLJ Markl Lindt "Hord
ö	<pre>chia coli. a; Proteobacteria; gamma subdivision; Enterobacteriaceae chia. xID=562;</pre>	
	1995 (Rel. 32, Created) 1995 (Rel. 32, Last sequence update) 1998 (Rel. 37, Last annotation update) brial major pilin protein (PRS pili) (Fragment).	DT 01-NOV-1995 (DT 01-NOV-1995 (DT 15-DEC-1998 (DEC-1998
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SEQUENCE FROM N.A.
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Lindberg F:, Gaastra W., Normark S.;
"Horizontal gene transfer of the Escherichia coli pap and prs
"Horizontal gene transfer the development of tissue-specific
operons as a mechanism for the development of tissue-specific
operons.";
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"Nucleotide sequence of the papA gene encoding of human uropathogenic Escherichia coli.";
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Baga M., Normark S., Hardy J., O'Hanley P.,
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SUBCELLULAR LOCATION: Secreted.
DISEASE: STRAINS OF E.COLI THAT CAUSE INFECTION OF THE HUMAN
URINARY TRACT PRODUCE PAP-PILI WHICH ARE HAIR-LIKE APPENDAGES
CONSISTING OF ABOUT 1000 HELICALLY ARRANGED SUBUNITS OF THE
PROTEIN PAPA. THESE PILI MEDIATE BINDING TO DIGALACTOSIDE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . Microbiol. 6:2225-2242(1992).
FUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5
MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO
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rPro; IPR000259; Fimbrial.
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                                                                                                                                                              PQGQGKVT 8
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8; Conserv
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185 AA;
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Last anotation (PAP pili).
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KS71A fimbrillin pre
KS71A.
                                                                                            FMK1_ECOLI
P04740;
13-AUG-1987
13-AUG-1987
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DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "DNA sequences of three papA genes from uropathogenic Escherichia coli strains: evidence of structural and serological conservation."; coli strains: evidence of structural and serological conservation."; coli strains: evidence of structural and serological conservation."; coli fect. Immun. 59:3849-3858(1991).

-i- PUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5

MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.

-i- DISEASE: THIS IS ONE OF THE FIMBRIAL PROTEINS INVOLVED IN MANNOSE-RESISTANT HEMAGGLUTINATION OF HUMAN ERYTHROCTYPES.
                                                                                                                                                                                                ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M12861; AAA23778.1; -. EMBL; M68060; AAA24278.1; -. PIR; A03496; YQECF2. PIR; B43597; B43597.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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P02972;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
01-NOV-1995 (Rel. 32, Last annotation
F7-2 fimbrial protein precursor (F7-2
F7-2 OR PAPA.
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Gene 32:83-90(1984).
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precursor (P-fimbrial antigen).
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coli
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SEQUENCE
EMBL; AL021546; CAA1
InterPro; IPR003837;
                                                              modified and this statement
                                                                                                                                                  Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases -!- SIMILARITY: BELONGS TO THE GATC FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
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                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhen M., van Die I., Rhen V., Bergmans H.;
"Comparison of the nucleotide sequences of the genes encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=85285072; PubMed=2992970;
                                        or send an
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Pfam; PF00419; Fimbrial;
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SIMILARITY: BELONGS TO THE FIMA/PAPA FAMILY OF FIMBRIA PROTEINS.
                                                                                              European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Blochem. 151:573-577(1985).
FUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR EILAMENTS RADIATING FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5
MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PQGQGKVT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                  PQGQGEVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an email to license@isb-sib.ch).
                                                                                                                                                                                             FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187
                                     equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                               Bioinformatics Institute. The profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                              STANDARD;
             CAA16496.1;
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                                                                                                                                                                                                                                    Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                license agreement (See http://www.isb-sib.ch/announce/
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1.2.
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75.0%;
 Glu-tRNAGln
                                                                   is not removed.
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KS71A FIMBRILLIN.
                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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01-MAR-2002 (Rel. 41, Last annotation update)
Runt-related transcription factor 2 (Core-binding subunit) (CBF-alpha 1) (Fragment).
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Hypothetical protein.
SEQUENCE 136 AA; 15086 MW;
                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no rest
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entities requires a license agreement (See http://www.isb-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Usemura T., Fu 2.W., Kato H.;
"Molecular cloning and expression of equine Cbfal.";
"Molecular cloning and expression of equine Cbfal.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
-I- FUNCTION: Transcription factor involved in osteoblas
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Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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01-MAR-2002 (Rel.
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SIMILARITY: CONTAINS 1 RUNT DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subunit binds DNA as a monomer and through the runt domain. binding is increased by heterodimerization (By similarity). SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        murine leukemia virus, polyomavirus enhancer, T-cell receptor enhancers, osteocalcin, osteopontin, bone sialoprotein, alpha 1(1) collagen, LCK, IL-3 and GM-CSF promoters (By similarity). SUBUNIT: Heterodimer of an alpha and a beta subunit. The alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                maturation of osteoblasts and both intramembranous and endochondral ossification. Cbf binds to the core site, 5'-proproger 3', of a number of enhances and promoters, including the contract of the core site of the core of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: Phosphorylated; probably by MAP kinases (MAPK)
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PQGQSQIT
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JUN2_HUMAN

STANDARD;

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RUN2_HUMAN

STANDARD;

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Q13950; O14614; O14615; O95181;

DT

O1-MAR-2002 (Rel. 41, Created)

DT

O1-MAR-2002 (Rel. 41, Last sequence update)

DT

O1-MAR-2002 (Rel. 41, Last sanotation update)

DE

Runt-related transcription factor 2 (Core-binding factor, alpha 1

DE

Subunit) (CBF-alpha 1) (Acute myeloid leukemia 3 protein) (Oncogene

AML-3) (Polyomavirus enhancer binding protein 2 alpha A subunit)

DE

(PEBP2-alpha A) (PEA2-alpha A) (SL3-3 enhancer factor 1 alpha A

DE

Subunit) (SL3/AKV core-binding factor alpha A subunit) (Osteoblast-

specific transcription factor 2) (OSF-2).
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Q40345;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
01-NOV-1997 (Rel. 35, Last ann
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Plant Mol. Biol. 20:801-807(1992).
-!- CATALYTIC ACTIVITY: Isocitrate + NADP(+) =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93099232; PubMed=1281435;
Shorrosh B.S., Dixon R.A.;
"Molecular characterization and expression of an isocitrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Medicago sativa (Alfalfa).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents
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SUBCELLULAR LOCATION: Chloroplast (Potential).
TISSUE SPECIFICITY: DEFECTED IN ALL TISSUES EXAMINED.
SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE
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REAL SERVICE S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Geoffroy V., Corral D.A., Zhou L., Lee B., Karsenty "Genomic organization, expression of the human CBFAI evidence for an alternative splicing event affecting function.";
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Eukaryota; Metazoa;
Mammalia; Eutheria;
patients.";
Gene 244:21-28(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The cDNA cloning of the transcripts of human to 6p12.3-p21.1, the locus for cleidocranial Oncogene 15:367-371(1997).
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                                                                                                                                                                              variability in c. Hum. Mol. Genet.
                                                                                                                                                                                                                                                           Gelb
                                                                                                                                                                                                                                                                         MEDLINE=20014723; PubMed=10545612; Zhou G., Chen Y., Zhou L., Thiruna
                                                                                                                                                                                                                                                                                                                                                                                             "Mutation analysis of core binding cleidocranial dysplasia.";
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MEDLINE=97351518; PubMed=9207800;
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                                          "PEBP2alphaA/CBFA1 mutations
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                                                                                                                     MEDLINE=20156388;
                                                                                                                                                                                                                                         Lee B.;
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                                                                             Y.-W., Yasui N., Kakazu N.,
a S., Ochi T., Okuzumi S., N
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                                                                                                                                                                                                                                                           Pirinen
                                                                                                                                                              in cleidocranial dysplasia."; enet. 8:2311-2316(1999).
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                                                                                                                                         SER-197
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Bae S.-C., Takahashi E.-I., Ito Y
Bae S.-C., Takahashi E.-I., Ito Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В.,
                                                                                                                                                                                                                                                           L., Thirunavukkarasu K., He Berry S.A., Greenberg C.R.,
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                   Transcription regulation; DNA-binding; Alternative splicing; Phosphorylation;
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                                                                                                                    InterPro;
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SUBUNIT: Heterodimer of an alpha and a beta subunit. The alpha subunit binds DNA as a monomer and through the Runt domain. DNA-binding is increased by heterodimerization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ossification of the calvaria), supernumerary teeth, short stature, and other skeletal changes. In some cases defects in RUNX2 are exclusively associated with dental anomalies.

SIMILARITY: CONTAINS 1 RUNT DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM:
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ALTERNATIVE PRODUCTS: 3 isoforms; 1/Cbfala (shown here), 2 and 3/Cbfalb; are produced by alternative splicing.
TISSUE SPECIFICITY: Specifically expressed in osteoblasts.
DOMAIN: A proline/serine/threonine rich region at the C-terminus is necessary for transcriptional activation of target genes and contains the phosphorylation sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISEASE: Defects in RUNX2 are the cause of cleidocranial dyspects. CCD), an autosomal dominant skeletal disorder with high penetrance and variable expressivity. It is due to defective endochondral and intramembranous bone formation. Typical feat include hypoplasia/aplasia of clavicles, patent fontanelles, wormian bones (additional cranial plates caused by abnormal
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DISEASE: De
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AF0011447; AAB65159.2;
AF0011445; AAB65159.2;
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AF0011448; AAB65159.2;
AF0011449; AAB65159.2;
AF0011449; AAB65159.2;
AF0011444; AAB65159.1;
AF0011445; AAB65158.1;
AF0011445; AAB65158.1;
AF0011446; AAB65158.1;
AF0011447; AAB65158.1;
AF0011448; AAB65158.1;
AF0011449; AAB65158.1;
AF0053949; AAC77441.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Transcription factor involved in osteoblastic differentiation and skeletal morphogenesis. Essential for the maturation of osteoblasts and both intramembranous and endochondral ossification. Cbf binds to the core site, 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                               IPR000040; AML1_Runt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          equires a license agreement (See http://www.isb-sib.ch/announce/
email to license@isb-sib.ch).
splicing;
101 228
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sa A., Patrono C., De Florio L., Velardo
Bertini E., Santorelli F.M.;
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                   Nuclear protein; ATP-binding; Polymorphism; Disease mutation
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Q08775; Q08776; Q35183; Q28237; Q9QUQ6; Q9ROU4; Q9QY29; Q9JLNU;
Q1-MAR-2002 (Rel. 41, Created)
Q1-MAR-2002 (Rel. 41, Last sequence update)
Q1-MAR-2002 (Rel. 41, Last annotation update)
Q1-MAR-2002 (Rel. 41, Last annotation update)
Runt-related transcription factor 2 (Core-binding factor, alpha 1 subunit) (CBF-alpha 1) (Acute myeloid leukemia 3 protein) (Oncoge AML-3) (Polyomavirus enhancer binding protein 2 alpha A subunit) (PEBP2-alpha A) (PEA2-alpha A) (S13-3 enhancer factor 1 alpha A subunit) (S13/AKV core-binding factor alpha A subunit) (Osteobla:
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Franceschi R.T.;

"MAPK pathways activate a transcription factor, Cbf
J. Biol. Chem. 275:4453-4
-i- FUNCTION: Transcripti
                                                                                               MEDLINE-97325751; PubMed-9182763; Komori T., Yagi H., Nomura S., Yamaguci Shimizu Y., Bronson R.T., Gao Y.-H., I. Kitamura Y., Yoshiki S., Kishimoto T.; "Targeted disruption of Cbfal results formation owing to maturational arrest formation owing to maturational arrest
                                                                                                                                                                                                                                         heterodimeric partner of a protein PEBP2 alpha."; Virology 194:314-331(1993).
                                                                                                                                                                                                                                                                                                                                                                                                             "Genomic structure and isoform expression Cbfal/Osf2 transcription factor."; Gene 214:187-197(1998).
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Cameron E., Onions D.E., Neil J.
"Proviral insertions induce the
                                                                                                                                                                                                                                                                                MEDLINE=93242761; PubMed=8386878; Ogawa E., Inuzuka M., Maruyama M. Ito Y., Shigesada K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CD2-MYC;
MEDLINE=97385157; PubMed=9238031;
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Cell 89:747-754(1997).
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MEDLINE=97325750; PubMed=9182762;
Ducy P., Zhang R., Geoffroy V., Ridall A.
"Osf2/Cbfal: a transcriptional activator
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                                       Xiao G., Jiang
Franceschi R.T
                                                          MEDLINE=20127938;
                                                                     PHOSPHORYLATION
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                                                                                                                                                                                                            STRAIN-129;
                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                             "Molecular cloning and characterization of PEBP2 beta, heterodimeric partner of a novel Drosophila runt-relat
                                                                                                                                                                                                                                                                                                               SEQUENCE OF
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Nakatsuka M., Komori T., Takada
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-98 | MEDLINE=99453726;
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Shigesada K., Ito Y.;
"PEBP2/PEA2 represents a family
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PRARRET RANGER R

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enhancers, osteocalcin, osteopontin, bone sialoprotei collagen, LCK, IL-3 and GM-CSF promoters.

SUBUNIT: Heterodimer of an alpha and a beta subunit subunit binds DNA as a monomer and through the Runt d binding is increased by heterodimerization.

SUBCELLULAR LOCATION: Nuclear.

ALTERNATIVE PRODUCTS: At least 9 isoforms; 1 (shown h 3/PEBP2-alpha A1, 4/PEBP2-alpha A2, 5/G1, 6/G2, 7/U1, 9/Y2; are produced by alternative splicing.

TISSUE SPECIFICITY: Found in thymus and testis, T cell TISSUE SPECIFICITY: Found in thymus and testis, T cell Tissue and testis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 differentiation and skeletal morphogenesis. Essential maturation of osteoblasts and both intramombers.
                                                                                                                                                                                                                                                                                                                                                                                     endochondral ossification. Cbf binds to the core site PYGPYGGT-3', of a number of enhancers and promoters,
                                                                                                                                                                                                                                                                                                                                              murine leukemia virus, polyomavirus enhancer, T-cell
                                                                                                                                                                                                                                                                                                                      bone sialoprotein,
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Runt domain.

(shown here), 32, 7/U1, 8/Y1

not in B-cell lines. Isoform 2 is exclusively particularly in osteoblasts; isoforms 3 and 4 cell lines; isoforms 5, 6, 7, 8 and 9 can be f and osteosarcoma cell lines. be found found in bone, are expressed T cell in skeletal osteoblasts lines in Tbut

DEVELOPMENTAL STAGE: Expression occurs early during skele development and is restricted to cells of the mesenchymal condensations and of the osteoblast lineage. Expression of the embryo reaches a poor lineage. 2 in the embryo reaches a peak at 12.5 days post-coitum.

DOMAIN: A proline/serine/threonine rich region at the C-tern is necessary for transcriptional activation of target genes contains the phosphorylation sites. C-terminus of isoform

PTM: Phosphorylated; probably by MAP SIMILARITY: CONTAINS 1 RUNT DOMAIN. kinases (MAPK).

entities requires s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr non-profit institutions as long as its content is d and this statement is not removed. Usage by and fc s requires a license agreement (See http://www.isb-sib.an email to license@isb-sib.ch). restrictions EMBL a collaboration for .ch/announce/ outstation no on way cial

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Transcription regulation; DNA-
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L; D14637; BAA05486.1; -.
L; AF010284; AAB5409.1; -.
L; AF05936; AAB82419.1; -.
L; AF053948; AAC77440.1; -.
L; AF053951; AAC78623.1; -.
L; AF053951; AAC78623.1; -.
L; AF134836; AAF22568.1; -.
L; AF134836; AAF22569.1; -.
L; AF031319; BAA85345.1; -.
L; AB013129; BAA85345.1; -.
L; AB013129; BAA85345.1; -.
L; AB013129; BAA85345.1; -.
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0853; Runt;
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MIHSPHKQPQNHKCGANFLQEDCKKALAFKWLISAGHYQPP
RPTESYSALTYWHAGIFKAASSIYNRCHKFYLEKKGCTMAS
NSLFSAVTPCQQSFFW -> MRIPV (IN ISOFORM 3
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ACTN2.

Homo sapiens (Human).

Homo sapiens (Human).

Homo sapiens (Human).

Horia; Metazoa; Chordata;

Horia; Primates;
                                                                                                                                                                                                                                                                                                                                  01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Alpha-actinin 2 (Alpha actinin skeletal muscle isoform cross linking protein).
                                                                                            Biochem. Biophys. Res. Commun. 265:256-259(1999).
                                                                                                                                   Tiso N., Majetti M.,
Danieli G.A.,
"Fine mapping and gen
                                                                                                                                                                                            "Cloning and characterization of two human skeletal muscle alphaactinin genes located on chromosomes 1 and 11.";
J. Biol. Chem. 267:9281-9288(1992).
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-Skeletal muscle;
MEDLINE-92250531; pubMed-1339456;
Beggs A.H., Byers T.J., Knoll J.H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN
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                                                                                                               the sarcomeric isoform of cardiac muscle.";
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                                                                                                                        mapping and genomic structure of ACTN2,
he sarcomeric isoform of alpha-actinin-2,
                                                                                                                                                                                                                           L.M.;
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M., Stanchi F., R
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MISSING (IN ISOFORM 7).

A -> S (IN REF. 4; AAC78

G -> S (IN REF. 4; AAC78

D -> N (IN REF. 4; AAC78

R -> T (IN REF. 4; AAC78

M -> L (IN REF. 4; AAC78

P -> L (IN REF. 4; AAC78

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R -> P (IN REF. 4; AAC78
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Pred. No.
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DDTATSDECLMPSSLSKKSQAGASELGPESDPRQFPSISSL
TESRESNPRMHYPATFTYTPPVTSGMSLGMSATTHYHTYLP
PPYPGSSQSQSGPFQTSTYLLYGTSSASYQFPMVPGGDR
SPSRMVPPCTTTSNGSTLLNPNLPNQNDGVDADGSHSSSPT
VLNSSGRMDESYMRPY --> SEPSTLDSQSSTTLFLSSEEP
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HERPQTMMAPAPALASERGHSQHAGPARDDHAEHPGTSPKP
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                                                                                                                                                     Rampazzo A.,
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                                                                                  STRUCTURES.
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                                                             forms heterodimers with
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                                                                                                                                                                                                        PROSITE; PS00020; ACTININ_2;
PROSITE; PS50021; CH; 2.
Actin-binding; Repeat; Multi
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HSSP; Q01082; 1BKR.
MIM; 102573; -
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; PF00435; spectrin; 4
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AJ249763;
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M86804; AAA51584.1;
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SPECTRIN 4.
EF-HAND 1 (POSSIBLY ANCESTRAL).
EF-HAND 2 (PROBABLY ANCESTRAL).
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SMART; SM00054; EFh; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Alpha-actinin 2 (Alpha actinin skeletal muscle isoform cross linking protein).
                                                                                                                                                                                                                                                                                                                        modified and this statement is not removentities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                This
                                                                                                                                                                                                                                      InterPro; IPR001589; Actinin_act_bind.
InterPro; IPR001715; Calponin_hom.
InterPro; IPR002048; EF-hand.
InterPro; IPR002017; Spectrin.
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[2]
                                                                        REPEAT
                                                                                      DOMAIN
                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                     between
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                                                                                                 DOMAIN
                                                                                                             DOMAIN
                                                                                                                       Actin-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: Homodimer, antiparallel. Also forms he ACTN3. Interacts with ADAMI2.
SIMILARITY: CONTAINS 1 ACTIN-BINDING DOMAIN.
SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) D
SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING
SIMILARITY: CONTAINS 4 SPECTRIN REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 275:13933-13939(2000).

EUNCTION: F-ACTIN CROSS-LINKING PROTEIN WHICH I
ACTIN TO A VARIETY OF INTRACELLULAR STRUCTURES.
                                                                                                                                                                                                                                                                                                                                                                      European Bioinformatics Institute.
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sen the Swiss Institute of Bioinformatics and the EM
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ACTININ_2;
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SPECTRIN 1.
SPECTRIN 2.
SPECTRIN 3.
SPECTRIN 4.
EF-HAND 1 (POSSIBLY ANCESTRAL).
EF-HAND 2 (PROBABLY ANCESTRAL).
MW; 4D707FE9FB31C5AC CRC64;
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                                                                                 ACTIN-BINDING.
CH 1.
CH 2.
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RESULT 12
AAC2_CHICK
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Best Local S
Matches 6
  HSSP; Q01082; IBKR.

Interpro; IPR001589; Actinin_act_bind.
Interpro; IPR0015175; Calponin_hom.
Interpro; IPR002046; EF-hand.
Interpro; IPR002017; Spectrin.
Pfam; PF00307; CH; 2.
Pfam; PF00036; efhand; 2.
Pfam; PF00035; spectrin; 4.
SMART; SM00053; EFh; 2.
SMART; SM00053; EFh; 2.
SMART; SM000510; SPEC; 2.
                                                                                                                                            EMBL; X13874; CAA32078.1; -. EMBL; X59247; CAA41935.1; -. PIR; S02032; S02032. PIR; S15481; S15481.
                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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1. FUNCTION: F-ACTIN CROSS-LINKING PROTEIN WHICH I: ACTIN TO A VARIETY OF INTRACELLULAR STRUCTURES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Primary structure of chicken skeletal actinins deduced from cDNA sequences."; Eur. J. Biochem. 177:649-655(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Galliformes; Phasianidae; Phasiani
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01-FEB-1991 (Rel. 17, Last sequ
01-MAR-2002 (Rel. 41, Last anno
Alpha-actinin 2 (Alpha actinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=89064821; I Arimura C., Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cross linking
                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                            PROTEIN.
SUBUNIT: HOMODIMER, ANTIPARALLEL.
SIMILARITY: CONTAINS 1 ACTIN-BINDING DOMAIN.
SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) E
SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING
SIMILARITY: CONTAINS 4 SPECTRIN REPEATS.
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i T., Yanagisawa
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RESULT 13
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                                                                      Fimbria; Signal.
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                                                                                                                                                                                                                                                            Amako K.;
                                                                                                                                                                                                                                                                             MEDLINE-88298666; PubMed-2900238;
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SIMILARITY: BELONGS TO THE FIMA/PAPA FAMILY OF FIMBRIA PROTEINS.
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ACTININ_2;
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
DNA Res. 5:55-76(1998).
-I- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES
-I- FUNCTION: FLAGELLA (BY SIMILARITY).
-I- SIMILARITY: BELONGS TO THE ARCHAEAL FLAGELLIN FAMILY.
                Streptococcus pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium
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Funahashi T., Tanaka T., Kudoh Y., Yamazaki
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb
Masuchi Y., Shizuya H., Kikuchi H.;
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Archaea; Euryarchaeota;
NCBI_TaxID=53953;
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Streptococcus
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Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A.,
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Search completed: October 28, 2002, Job time: 7.89474 secs
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RA Tettelin H., Nelson K.E., Paulsen I.T., Haft D.H., Dodson R.J.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Durkin A.S., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angluoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Holt I.E., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT "pneumoniae.",
Sclence 293:498-506(2001).
CC diphosphate + UDP-glucose.
-i- STALLARITY: BELONGS TO THE PROKARYOTIC UDPGP FAMILY.
-i- STALLARITY: BELONGS TO THE PROKARYOTIC UDPGP FAMILY.
                                                                                                                                                                                 Query Match
Best Local S
Matches 5
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                                                                                                                                                                                                                                                                       InterPro; IPR001825; NTP_transferase.
Transferase; Kinase; Nucleotidyltransferase; Complete proteome.
SEQUENCE 299 AA; 33278 MW; E9D644167B4356C3 CRC64;
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[1]
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les 5; Conservative
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Gapop 10.0 , Gapext 0.5
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ALIGNMENTS

AC QS DT 01 DT 01 DT 01 DT 01	SUL R8B	Qy Db	Query Best Match	SQ SE				SUL R53
Q9R8B2; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) PAPA (FRAGMENT).	T 2 2 Q9R8B2 PRELIMINARY; PRT; 137 AA.	1 PQGQGKVT 8 2 PQGQGKVT 9	Query Match 100.0%; Score 43; DB 2; Length 30; Best Local Similarity 100.0%; Pred. No. 0.15; Mismatches 0; Indels 0; Gaps 0;	J. Bacteriol. 175:7391-7403(1993). SEQUENCE 30 AA; 2964 MW; 5F63B427E63FFA90 CRC64;	SEQUENCE. MEDLINE-94042915; PubMed-7901197; Giron J.A., Ho A.S., Schoolnik G.K.; Characterization of fimbriae produced by enteropathogenic Escherichia	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Bscheriohia. NCBI_TaxID-562; [1]	01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2000 (TrEMBLrel. 14, Last annotation update) 15.5 KDA FIMBRIAL SUBUNIT (FRAGMENT).	T 1 0 0 09R530 PRELIMINARY; PRT; 30 AA.

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"Genomic analysis of a pathogenicity island in uropathogenic Escherichia coli CFT073; distribution of homologous sequences isolates from patients with pyelonephritis, cystitis, and cat associated bacteriuria and from fecal samples.";

Infect. Immun. 66:4411-4417(1998).

EMBL; AF081285; AAC61718.1; -.

InterPro; IPR001259; Fimbrial.

Pfam; PF00419; Fimbrial; 1.
                                                                                                                                                                                                          Johnson J.R., Stell A.L.; "The papa Variant F48 in Previously F-type Negative Escherichia Strains.";
                                                                                                                                                                          Submitted (MAR-2000) to the EMBL/GenBank/DDBJ EMBL; AF250040; AAG00915.1; -. NON_TER 1 1
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PAPA VARIANT F48 (FRAGMENT).
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Escherichia
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llarity 100.0%;
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pyelonephritogenic Escherichia
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SEQUENCE
                                                                                                                                                              Johnson J.R., Delavari P., Kuskowski M., Stell A.L.; Phylogenetic distribution of extraintestinal virulence-associated traits in Escherichia coli."; J. Infect. Dis. 183:78-88 (2001). EMBL; AF247354; AAF97911.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Johnson J.R., Stell A.L., Schuetz F., O'Bryan T.T., Russo T.A., Carlino U.B., Fasching C., Kavle J., Van Dijk L., Gaastra W.; "Analysis of the Fantigen-specific papa alleles of extraintestinal pathogenic escherichia coli using a novel multiplex PCR-based assay Infect. Immun. 68:1587-1599(2000).
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01-FEB-1997 (TrEMBLrel. 02,
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Bacteria; Proteobacteria;
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Johnson J.R., Delavari P., Kuskowski M.,
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SEQUENCE
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EMBL; AF332520; AAK11634.1; -.
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Johnson J.R., O'Bryan T.T., Kuskowski M., Maslow J.N.;
"Ongoing Horizontal and Vertical Transmission of Virulence Genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Johnson J.R., Delavari P., Kuskowski M., Stell A.L.;
"Phylogenetic distribution of extraintestinal virulence-associated traits in Escherichia coll.";
J. Infect. Dis. 183:78-88 (2001).
EMBL; AF247357; AAF97914.1; -.
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Bacteria; Proteobacteria;
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EMBL; AF051815; AAD02666.1; -.
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SEQUENCE FROM N
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Parteria; Proteobacteria;
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Boyd E.F., Hartl D.L.;
"Diversifution and account of the control of the contr
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SEQUENCE FROM N.A.
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STRAIN-ECOR 53, ECOR 48,
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8; Conserv
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Q9KHX4;
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Johnson J.R., Stell A.L., Schuetz F., O'Bryan T.T., Russo T.A.,
Johnson J.R., Stell A.L., Schuetz F., O'Bryan T.T., Russo T.A.,
Carlino U.B., Fasching C., Kavle J., Van Dijk L., Gaastra W.;
"Analysis of the F antigen-specific papa alleles of extraintestinal pathogenic escherichia coll using a novel multiplex PCR-based assay.";
Infect. Immun. 68:1587-1599(2000).
EMBL; Y08927; CAA70131.1;
InterPro; IPR000259; Finbrial.
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Pacteria; Proteobacteria;
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
F10 P-FIMBRIAE MAJOR SUBUNIT PRECURSOR.
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                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Johnson J.R., Delavari P., Kushowski M., Stell
"Phylogenetic Distribution of Extraintestinal
Traits in Escherichia coli.";
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POTENTIAL.
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Pred. No. 0.97;
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tinal Virulence-Associated
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                        Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                              Johnson J.R., Delavari P., Kuskowski M., Stell A.L.; "Phylogenetic distribution of extraintestinal virulence-associated traits in Escherichia coli.";
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Search completed: October 28, 2002, 17:24:03 Job time : 20.5263 secs
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STRAIN-ECOR 24;

MEDLINE-21062863; PubMed-11106538;

Johnson J.R., Delavari P., Kuskowski M., Stell A.L.;

Johnson J.R., Delavari P., Kuskowski M., Stell A.L.;

"Phylogenetic distribution of extraintestinal virulence-associated traits in Escherichia coll.";

J. Infect. Dis. 183:78-88(2001).

EMBL; AF247346; AAF97903.1; -.

SEQUENCE 177 AA; 18171 MW; 822C14624B5DE8C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         O9KHX2;
O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ADHESION PROTEIN PAPA.
Escherichia coli.
                                                                                                                                                                                                   Johnson J.R., Delavari P., Kuskowski M., Stell A.L.;
"Phylogenetic distribution of extraintestinal virulence-associated traits in Escherichia coll.";
J. Infect. Dis. 183:78-88(2001).
EMBL; AF247353; AAF97910.1;
SEQUENCE 177 AA; 18143 MW; E95C03D49033ADD5 CRC64;
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STRAIN-ECOR 56;
MEDLINE-21062863; PubMed-11106538;
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NCBI_TaxID=562;
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Drosophila melanog	ABB59904	22	1189	0	35	43
	AAB86165	22	1179	0.	35	42
Human MTR1 protein	AAB86162	22	1165	60.3	35	41
Mouse MTR1 protein	AAB86166	22	1158	0.	35	40
MTR1	AAB86164	22	1158	60.3	3 <u>5</u>	39
Defective retrovir	AAB73284	22	1069	0	35	38
Human MTR1 protein	AAB86163	22	872	0	35	37
Human polypeptide	AAM41064	22	809	0.	35	36
PERV-A env protein	AAB35113	22	660	0	35	35
a	AAB70632	22	660	0	35	34
Pig endogenous ret	AAW85453	20	660	0	35	33
cin	AAW32095	18	657	0.	35	32
Novel human diagno	ABG27471	22	652		35	31
Drosophila melanog	ABB59450	22	648		35	30
\vdash	AAB70637	22	221	0.	35	29
	AAB16428	21	116	60.3	35	28
	ABB67899	22	113	0	35	27
Drosophila melanog	ABB71328	22	886	2	36	26
eri	AAB79357	22	637	2	36	25
C glutamicum prote	AAG89928	22	576		36	24
o	AAW70505	19	388	2	36	23
Human immune/haema	AAM88679	22	198		36	22
Bacterial P pilus	AAB72835	22	163	2	36	21
Pilin protein, Pap	AAB47081	22	163	2	36	20
U849	AAP60247	7	163		36	19
Sequence of the Ga	AAP50045	σ	163		36	18
Human polypeptide	AAO00501	22	142		36	17
Human polypeptide	AA000939	22	137	62.1	36	16
Amino acid sequenc	ААВ19198	21	131	2	36	15
	0910	22	71	۲	36	14
H	76	22	989	63.8	37	13
Drosophila melanog	ABB67212	22	7	ω.	37	12

ALIGNMENTS

RESULT 1 ABG09511

13-FEB-2002 (first entry)

Novel human diagnostic protein #9502

ABG09511;

ABG09511 standard;

Protein;

449

A

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess WPI; 2001-639362/73. N-PSDB; AAS73698. Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder. Drmanac RT, Liu C, 31-MAR-2000; 2000US-0540217 23-AUG-2000; 2000US-0649167 30-MAR-2001; 2001WO-US08631 11-OCT-2001. WO200175067-A2 Homo sapiens. (HYSE-) HYSEQ INC.

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RESULT 2
ABG08528
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Consider the sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                           biodiversity
                                                                                                                                                                                         N-PSDB; AAS72715.
                                                                                                                                                                                                                        WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                        (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US08631
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nes 7; Conserv
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                                                                                                                                                                                                                                                                                        RT,
                                                                                                                                                                                                                                                                                                                                                        OBSAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                     Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      relates to isolated polynucleotide (I) and II) sequences. (I) is useful as hybridisation probes.
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                                                                                                                                                                                                                                                                                                                                                            INC.
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                                                                                                                                                                                                                                                                                        Tang YT;
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Pred. No.
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ches 3;
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The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC the polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations are responsible for genetic disorders or other traits to assess biodiversity amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed content of the major of the invention.
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Matches
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                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                  WPI; 2001-639362/73.
N-PSDB; AAS73690.
                                                                                                                                                                                                                                                 31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human diagnostic protein #9494.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG09503;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at ftp.wipo.int/pub/published_pct_sequences.
             Claim 20; SEQ ID No 39862; 103pp; English
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                                                                                                                                                                                                                   HYSEQ INC
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ches 3;
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RESULT 4
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Best Local
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes,
                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
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23-AUG-2000;
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N-PSDB; AAS77017.
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                                                                                                                    Claim 20; SEQ ID No 43189; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu C,
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2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mapping; gene mapping; gene therapy; forensic;
medical imaging; diagnostic; genetic disorder.
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63.6%;
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Pred. No. 1.2e+02;
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temperature transition. Abductin

present sequence represents a bay scallop abductin polypeptide polypeptide is capable of chemomechanical transduction or inver

polypeptides

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RESULT 5
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Best Local S
                                                                                                   Abductin nucleic acid molecules, useful for expressing polypeptides which are used in the manufacture of drug vehicles for administering water soluble drugs -
                                                                                                                                                                                                                            Bayley H,
                                                                                                                                                                                                                                                             (BAYL/) BAYLEY H. (CAOQ/) CAO Q. (WANG/) WANG Y.
                                                                                                                                                                                                                                                                                                                                   03-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bay scallop; abductin; chemomechanical transduction; drug delivery;
inverse temperature transition; water soluble drug; biomaterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB19197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polymerase chain reaction (PCR) primers, oligomers, and and gene mapping, and in recombinant production of (II).
                                                                    Example 1; Fig 2;
                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                           WPI; 2000-611057/58.
                                                                                                                                                                                                                                                                                                                                                                      03-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                          US6127166-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fabric;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of a bay scallop abduction polypeptide
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                                                                                                                                                                            AAC61378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organ prosthesis.
                                                                                                                                                                                                                            Cao Q,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          536 AA;
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                                                                    30pp; English.
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63.6%;
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Pred. No. 1.4e+02;
1; Mismatches 3
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                                                                                                                       abductin
delivery
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9199
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(CAOQ/) CAO Q.
(WANG/) WANG Y.
                                                                                    The present sequence represents a bay scallop abductin polypeptide. The polypeptide is capable of chemomechanical transduction or inverse temperature translition. Abductin polypeptides contain glycine-rich sequences. Abductin polypeptides are useful in the manufacture of drug delivery vehicles for administering water soluble drugs. The abductin polypeptides and their derivatives are also useful in the manufacture of broad range of biomaterials ranging from light-weight durable fabric for clothing to matrices useful for human tissue and
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                                                                                                                                                                                                                              Abductin nucleic acid molecules, useful for expressing polypeptides which are used in the manufacture of drug vehicles for administering water soluble drugs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bay scallop; abductin; chemomechanical transduction; drug delivery; inverse temperature transition; water soluble drug; biomaterial; fabric; organ prosthesis.
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                                                                                                                                                                                                                                                                                   N-PSDB; AAC61380
                                                                                                                                                                                                                                                                                                                       Bayley H, Cao Q,
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                                                   Sequence
                                                                                                                                                                                                        Example 1; Fig
                                                                                                                                                                                                                                                                                                                                                                                                   03-NOV-1997;
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 Similarity 7; Conserv
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  Conservative
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                                                                                                                                                                                                                                                                                                                       Wang
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77.8%;
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           Score 38;
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56;
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RESULT 8
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AC AAY8
AC AAY8
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AC AAY8
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Best Local S
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(CAOQ/) CAO Q.
(WANG/) WANG Y.
                                                                                                                                                                                                                                  abductin polypeptides and their derivatives are also useful in the manufacture of broad range of biomaterials ranging from light-weight durable fabric for clothing to matrices useful for human tissue and
                                                                                                                                                                                                                                                                The present sequence represents a bay scallop abductin polypeptide. The polypeptide is capable of chemomechanical transduction or inverse temperature transition. Abductin polypeptides contain glycine-rich sequences. Abductin polypeptides are useful in the manufacture of drug delivery vehicles for administering water soluble drugs. The
                                                                                                                                                                                                                                                                                                                                                         Abductin nucleic acid molecules, useful for expressing polypeptides which are used in the manufacture of drug vehicles for administering water soluble drugs -
                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bay scallop; abductin; chemomechanical transduction; drug delive inverse temperature transition; water soluble drug; biomaterial;
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                                                       AAY80088 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fabric; organ prosthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of a bay scallop abduction polypeptide
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                                                                                                             FGGMGGGKG
                                                                                                                                                                                                                         prostheses.
                                                                                                                                                       l Similarity
7; Conserv
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                                                       Protein;
                                                                                                                                                                  65.5%;
77.8%;
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                                                                                                                                                        Score 38; DB Pred. No. 60; 0; Mismatches
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16-MAY-2000 AAY80088;

(first entry)

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RESULT 9
ABB67213
ID XX
ABB6
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ABB6
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ABB6
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ABB6
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ABB6
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DT 26-M
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      molecules can degrade or transport fumonisin and can reduce the pathogenicity of a fungus producing fumonisin. The plants may be e.g. maize, sorghum, wheat, tomato, soybean, alfalfa, sunflower, Brassica, cotton or rice. The products can also be used as detection reagents for fumonisins and related compounds. AAZ91253 represents the Bacterium 2412.1 fumonisin catabolic gene cluster, and AAZ91254 to AAZ91273 represent isolated nucleic acids from Bacterium 2412.1 which encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid molecules which encode fumonisin degradative enzymes and transporters, used for detoxifying fumonisin or related mycotoxin or reducing the pathogenicity of fungi producing fumonisin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY80085 to AAY80104. AAZ91286 to AAZ91291 represent sequence used in the exemplification of the present invention. AAZ91274 to AAZ91285 are given in the sequence listing from the present specification but are not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 106-108; 181pp; English.
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                   Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical.
                                                                         Drosophila melanogaster polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specifically mentioned
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                                                                                                                   26-MAR-2002
                                                                                                                                                        ABB67213;
                                                                                                                                                                                            ABB67213 standard; Protein;
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Pred. No.
2; Mismatc
                                                                                                                                                                                            574 AA
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                                                                           SEQ ID NO 28431.
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1.9e+02;
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                              Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster polypeptide SEQ ID NO 21735.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO
                 (PEKE ) PE CORP NY
                                                       23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent
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11-JUL-2000;
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DB; ABL11316.
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                                                                                                                                                                                                                                                                                      developmental biology; cell signalling; insecticide;
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2000US-0614150
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70.0%;
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   capable
                   The invention
                                                                                                                                                                                                                                                                                                   23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster polypeptide SEQ ID NO 23991.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB65733 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid genes from Drosophila and
                                                       Disclosure;
                                                                                                           New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                   WPI; 2001-656860/75.
N-PSDB; ABL09836.
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ion relates to an idetecting 1000 or
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                                                       SEQ ID NO
                                                                                                                                                                                                                         Adams M,
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2000US-0614150.
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                                                                                                                                                                                                                           PWD,
                                                                                                           detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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                   isolated
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Pred. No. 3.3e+02;
Pred. No. 3.3e+02;
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                                                    21pp + Sequence Listing; English.
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genes
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 nucleic
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acid detection reagent Drosophila. The invention
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RESULT 12
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ID ABB67
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                                                                                   capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins
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                       (ABB57737-ABB72072) The sequence data f specification, but
                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO
                                                                                                                                                                                                                                                                                                                 interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PEKE )
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ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 developmental biology;
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2000US-0614150
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                                            for this patent did not form
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70.0%;
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                                                                                                                                                                                                                                                                                                                                      detection reagent for detecting for elucidating cell signalling
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3.3e+02;
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DB 22;

Length 578;

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                                                                                                                      RESULT 14
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Matches 7; Conservative
                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                              The present invention provides the protein and coding sequences of a number of human shear stress response proteins. These are useful in diagnosis, treatment and screening of vascular diseases caused by arteriosclerosis, including heart failure, post-PTCA restenosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arteriosclerosis
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                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                  Claim 60; Page 284-288; 678pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                       DNA sequences, proteins encoded by them and antibodies against them useful in diagnosis and treatment of vascular disease caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAH02892.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nojima H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-OCT-2000; 2000WO-JP06840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human shear stress-response protein SEQ ID NO:
           Human polypeptide SEQ ID NO 22996
                                       06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kuga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                             AAO09104 standard; Protein;
                                                                                                                                                                                                                                                                                                  hypertension.
                                                                                                                                                                                                                                                                                                                                                                                                             arteriosclerosis -
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(NOJI/) NOJIMA H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2001 (first entry)
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545 RFGGGGFKKG 554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         shear stress-response protein; vascular disease;
                                                                                                                                                                                                                  Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         yoshisue Sekine S,
                                                                                                                                                                                                                                                                          989 AA;
                                                                                                                                                                                                                  Conservative
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Nakamura
                                                                                                                                                                                                                               63.8%;
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                                                                                                                                                                                                                  Score 37; DB
Pred. No. 5.4e
1; Mismatches
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1; Mismatches 2;
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                                                                                                                                                                                                                    .4e+02;
es 2;
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                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating
                                                                 inverse fabric;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                            Bay scallop; abductin; chemomechanical transduction; drug delivery; inverse temperature transition; water soluble drug; biomaterial;
                                                                                                                                                                                                    AAB19198 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activity, tissue growth factor activity, immunomodulatory activity activin/inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID NO 22996; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                       Argopecten sp
                                                                                                                     Amino acid sequence of a bay scallop abduction polypeptide
                                                                                                                                                 19-FEB-2001
                                                                                                                                                                            AAB19198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-FEB-2001; 2001WO-US04927
                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammation.
                                                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                        3 FGGMGAKKG 11
                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                        FGGGGLKKG
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                                                                                                                                                                                                                                                                                                                           Similarity 7; Conserv
                                                                 organ prosthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu C,
                                                                                                                                                                                                                                                                                                                                                                                  71 AA;
                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                (first
                                                                                                                                                                                                                                                                          71
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                                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                         62.1%;
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                                                                                                                    Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BAYL/) BAYLEY H. (CAOQ/) CAO Q. (WANG/) WANG Y.
                                                                                                                                                                                                                              The present sequence represents a bay scallop abductin polypeptide. The polypeptide is capable of chemomechanical transduction or inverse temperature transition. Abductin polypeptides contain glycine-rich sequences. Abductin polypeptides are useful in the manufacture of drug delivery vehicles for administering water soluble drugs. The abductin polypeptides and their derivatives are also useful in the manufacture of broad range of biomaterials ranging from light-weight durable fabric for clothing to matrices useful for human tissue and
                                                                                                                                                                                                                                                                                                                                                                                                   Abductin nucleic acid molecules, useful for expressing abductin polypeptides which are used in the manufacture of drug delivery vehicles for administering water soluble drugs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-611057/58.
N-PSDB; AAC61379.
                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 2; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-OCT-2000.
                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                  organ prostheses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bayley H, Cao Q, Wang Y;
                                                          3 FGGMGAKKG 11
                                                                                                                                                                                     131 AA;
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                                                                                                                                      62.1%;
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